

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser	Ser	Pro	Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys
1				5					10					15	

Pro Ala

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu
1				5					10	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Phe Arg Ile Phe Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe
1 5 10 15

Asp Ala Cys Gly Phe
20

- (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly
1 5 10 15

Tyr Ser Thr Ser Leu
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	Leu	His
1				5					10					15	
Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe	Met	Leu
			20					25					30		
Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	Glu	Gln
		35					40					45			
Asp	Ser														
	50														

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser	Thr	Val	Glu	Cys	Lys	Ala	Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val
1				5				10						15	
Val	Ser	Asn	Tyr	Phe	Trp	Leu	Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr
		20						25					30		
Leu	Leu	Val	Glu	Thr	Phe	Phe	Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr
		35					40					45			
Thr	Ile	Ile	Gly	Trp	Gly	Thr	Pro	Thr	Val	Cys	Val				
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr	Ala	Leu	Trp	Trp	Val	Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met
1				5					10					15	
Val	Asn	Phe	Val	Leu	Phe	Ile	Gly	Ile	Ile						
			20					25							

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met	Gly	Gly	Asn	Glu	Ser
1				5					10					15	
Ser	Ile	Tyr													

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro	Leu	Phe	Gly	Ile
1				5					10					15	

His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu
 20 25 30
 Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val
 35 40 45
 Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys
 50 55 60
 Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe
 65 70 75

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly
 1 5 10 15
 Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met
 20 25 30
 Ser

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu
 1 5 10 15
 Lys Ile Gln Arg Val Asn Asp Leu Met Gly Leu Asn Asp
 20 25

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu	1	5	10	15
Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	Asn	Asp	Ser	Ser	Pro	20	25	30	
Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	Pro	Ala	His	35	40	45	
Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Leu	Phe	Arg	Ile	Phe	50	55	60	
Asn	Pro	Asp	Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	Gly	Glu	Phe	Gly	Phe	65	70	75	
Ala	Asp	Ser	Lys	Ser	Leu	Asp	Leu	Ser	Asp	Met	Arg	Val	Val	Ser	Arg	85	90	95	
Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	Tyr	Phe	Asp	100	105	110	
Ala	Cys	Gly	Phe	Glu	Glu	Tyr	Glu	Ser	Glu	Thr	Gly	Asp	Gln	Asp	Tyr	115	120	125	
Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	130	135	140	
Leu	Val	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	145	150	155	
Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe	165	170	175	
Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	180	185	190	
Glu	Gln	Asp	Ser	Asn	His	Cys	Phe	Val	Ser	Thr	Val	Glu	Cys	Lys	Ala	195	200	205	

Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu
210						215					220				
Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe
225					230					235					240
Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Ile	Ile	Ile	Gly	Trp	Gly	Thr
				245					250					255	
Pro	Thr	Val	Cys	Val	Ser	Val	Trp	Ala	Met	Leu	Arg	Leu	Tyr	Phe	Asp
			260					265					270		
Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Asn	Thr	Ala	Leu	Trp	Trp	Val
		275					280					285			
Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe
	290					295					300				
Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met
305					310					315					320
Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Ser	Cys	Val	Gln	Lys	Cys	Tyr
				325					330					335	
Cys	Lys	Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu
			340					345					350		
Ser	Thr	Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro
		355					360					365			
Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro	Glu	Asn	Val
	370					375					380				
Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	Gly	Ser	Phe	Gln
385					390					395					400
Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn	Gly	Glu	Val	Gln
				405					410					415	
Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	Asn	Arg	Tyr	Phe
			420					425					430		
Thr	Met	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala	Ser	Ser	Gly	Val
		435					440					445			
Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser	Ser	Ser	Gln	Ile
	450					455					460				
Arg	Met	Ser	Gly	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr				
465					470					475					

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 513 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Arg	Gly	Gly	Arg	His	Trp	Pro	Glu	Pro	Pro	Cys	Arg	Leu	Arg	Ser	1	5	10	15
Val	Met	Ala	Ser	Ile	Ala	Gln	Val	Ser	Leu	Ala	Ala	Leu	Leu	Leu	Leu	20	25	30	
Pro	Met	Ala	Thr	Ala	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	35	40	45	
Ala	Met	Cys	Leu	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	50	55	60	
Asn	Asp	Ser	Ser	Pro	Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	65	70	75	
Trp	Lys	Pro	Ala	His	Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	85	90	95	
Leu	Phe	Arg	Ile	Phe	Asn	Pro	Asp	Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	100	105	110	
Gly	Glu	Phe	Gly	Phe	Ala	Asp	Ser	Lys	Ser	Leu	Asp	Leu	Ser	Asp	Met	115	120	125	
Arg	Val	Val	Ser	Arg	Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	130	135	140	
Pro	His	Tyr	Phe	Asp	Ala	Cys	Gly	Phe	Glu	Glu	Tyr	Glu	Ser	Glu	Thr	145	150	155	
Gly	Asp	Gln	Asp	Tyr	Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	165	170	175	
Gly	Tyr	Ser	Thr	Ser	Leu	Val	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	180	185	190	
Cys	Arg	Phe	Arg	Lys	Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	195	200	205	
Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	210	215	220	

Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His Cys Phe Val Ser Thr
 225 230 235 240
 Val Glu Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser
 245 250 255
 Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu
 260 265 270
 Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Ile Ile
 275 280 285
 Ile Gly Trp Gly Thr Pro Thr Val Cys Val Ser Val Trp Ala Met Leu
 290 295 300
 Arg Leu Tyr Phe Asp Asp Thr Gly Cys Trp Asp Met Asn Asp Asn Thr
 305 310 315 320
 Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met Val
 325 330 335
 Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu
 340 345 350
 Gln Ser Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys
 355 360 365
 Val Gln Lys Cys Tyr Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys
 370 375 380
 Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr
 385 390 395 400
 Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe
 405 410 415
 Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly
 420 425 430
 Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu
 435 440 445
 Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys
 450 455 460
 Val Asn Arg Tyr Phe Thr Met Asp Phe Lys His Arg His Pro Ser Leu
 465 470 475 480
 Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys
 485 490 495
 Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala

500

505

510

Thr

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu
1 5 10 15

Lys Ile Gln Arg Val Asn Asp Leu Met Gly Leu Asn Asp Ser Ser Pro
20 25 30

Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His
35 40 45

Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe
50 55 60

Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe
65 70 75 80

Ala Asp Ser Lys Ser Leu Asp Leu Ser Asp Met Arg Val Val Ser Arg
85 90 95

Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp
100 105 110

Ala Cys Gly Phe Glu Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr
115 120 125

Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser
130 135 140

Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys
145 150 155 160

Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe
165 170 175

Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala

180										185				190			
Glu	Gln	Asp	Ser	Asn	His	Cys	Phe	Val	Ser	Thr	Val	Glu	Cys	Lys	Ala		
		195					200					205					
Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu		
	210					215					220						
Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe		
225					230					235					240		
Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Ile	Ile	Ile	Gly	Trp	Gly	Thr		
				245					250					255			
Pro	Thr	Val	Cys	Val	Ser	Val	Trp	Ala	Met	Leu	Arg	Leu	Tyr	Phe	Asp		
			260					265					270				
Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Asn	Thr	Ala	Leu	Trp	Trp	Val		
		275					280					285					
Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe		
	290					295					300						
Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met		
305					310					315					320		
Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu		
				325					330					335			
Leu	Leu	Ile	Pro	Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser		
			340					345					350				
Pro	Glu	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu		
		355					360					365					
Gly	Ser	Phe	Gln	Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn		
	370					375					380						
Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val		
385					390					395					400		
Asn	Arg	Tyr	Phe	Thr	Met	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala		
				405					410					415			
Ser	Ser	Gly	Val	Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser		
			420					425					430				
Ser	Ser	Gln	Ile	Arg	Met	Ser	Gly	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr		
		435					440					445					

160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Arg	Gly	Gly	Arg	His	Trp	Pro	Glu	Pro	Pro	Cys	Arg	Leu	Arg	Ser	1	5	10	15
Val	Met	Ala	Ser	Ile	Ala	Gln	Val	Ser	Leu	Ala	Ala	Leu	Leu	Leu	Leu	20	25	30	
Pro	Met	Ala	Thr	Ala	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	35	40	45	
Ala	Met	Cys	Leu	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	50	55	60	
Asn	Asp	Ser	Ser	Pro	Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	65	70	75	
Trp	Lys	Pro	Ala	His	Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	85	90	95	
Leu	Phe	Arg	Ile	Phe	Asn	Pro	Asp	Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	100	105	110	
Gly	Glu	Phe	Gly	Phe	Ala	Asp	Ser	Lys	Ser	Leu	Asp	Leu	Ser	Asp	Met	115	120	125	
Arg	Val	Val	Ser	Arg	Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	130	135	140	
Pro	His	Tyr	Phe	Asp	Ala	Cys	Gly	Phe	Glu	Glu	Tyr	Glu	Ser	Glu	Thr	145	150	155	
Gly	Asp	Gln	Asp	Tyr	Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	165	170	175	
Gly	Tyr	Ser	Thr	Ser	Leu	Val	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	180	185	190	
Cys	Arg	Phe	Arg	Lys	Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	195	200	205	
Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	210	215	220	

Asp Asn Leu Ala Thr
485

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu
 1 5 10 15

Arg Ile Gln Arg Ala Asn Asp Leu Met Gly Leu Asn Glu Ser Ser Pro
 20 25 30

Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala Gln
 35 40 45

Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Val Phe Arg Ile Phe
 50 55 60

Asn Pro Asp Gln Val Trp Met Thr Glu Thr Ile Gly Asp Ser Gly Phe
 65 70 75 80

Ala Asp Ser Asn Ser Leu Glu Ile Thr Asp Met Gly Val Val Gly Arg
 85 90 95

Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp
 100 105 110

Ala Cys Gly Phe Asp Asp Tyr Glu Pro Glu Ser Gly Asp Gln Asp Tyr
 115 120 125

Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser
 130 135 140

Leu Ala Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys
 145 150 155 160

Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe
 165 170 175

Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala
 180 185 190

Glu Gln Asp Ser Ser His Cys Phe Val Ser Thr Val Glu Cys Lys Ala
 195 200 205

Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu
 210 215 220

Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe
 225 230 235 240
 Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr
 245 250 255
 Pro Thr Val Cys Val Thr Val Trp Ala Val Leu Arg Leu Tyr Phe Asp
 260 265 270
 Asp Ala Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val
 275 280 285
 Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe
 290 295 300
 Ile Gly Ile Ile Ile Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met
 305 310 315 320
 Gly Gly Asn Glu Ser Ser Ile Tyr Leu Arg Leu Ala Arg Ser Thr Leu
 325 330 335
 Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser
 340 345 350
 Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu
 355 360 365
 Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn
 370 375 380
 Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val
 385 390 395 400
 Asn Arg Tyr Phe Thr Met Asp Phe Lys His Arg His Pro Ser Leu Ala
 405 410 415
 Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser
 420 425 430
 Ser Ser Gln Leu Arg Met Ser Ser Leu Pro Ala Asp Asn Leu Ala Thr
 435 440 445

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

[illegible]

Met	Ala	Arg	Val	Leu	Gln	Leu	Ser	Leu	Thr	Ala	Leu	Leu	Leu	Pro	Val	1	5	10	15
Ala	Ile	Ala	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	20	25	30	
Cys	Leu	Glu	Arg	Ile	Gln	Arg	Ala	Asn	Asp	Leu	Met	Gly	Leu	Asn	Glu	35	40	45	
Ser	Ser	Pro	Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	50	55	60	
Pro	Ala	Gln	Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Val	Phe	65	70	75	80
Arg	Ile	Phe	Asn	Pro	Asp	Gln	Val	Trp	Met	Thr	Glu	Thr	Ile	Gly	Asp	85	90	95	
Ser	Gly	Phe	Ala	Asp	Ser	Asn	Ser	Leu	Glu	Ile	Thr	Asp	Met	Gly	Val	100	105	110	
Val	Gly	Arg	Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	115	120	125	
Tyr	Phe	Asp	Ala	Cys	Gly	Phe	Asp	Asp	Tyr	Glu	Pro	Glu	Ser	Gly	Asp	130	135	140	
Gln	Asp	Tyr	Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	145	150	155	160
Ser	Thr	Ser	Leu	Ala	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	165	170	175	
Phe	Arg	Lys	Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	180	185	190	
Val	Ser	Phe	Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	195	200	205	
Leu	Tyr	Ala	Glu	Gln	Asp	Ser	Ser	His	Cys	Phe	Val	Ser	Thr	Val	Glu	210	215	220	
Cys	Lys	Ala	Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	225	230	235	240
Phe	Trp	Leu	Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	245	250	255	
Thr	Phe	Phe	Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly				

260	265	270
Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala Val Leu Arg Leu		
275	280	285
Tyr Phe Asp Asp Ala Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu		
290	295	300
Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe		
305	310	315
Val Leu Phe Ile Gly Ile Ile Ile Ile Leu Val Gln Lys Leu Gln Ser		
	325	330
Pro Asp Met Gly Gly Asn Glu Ser Ser Ile Tyr Leu Arg Leu Ala Arg		
	340	345
Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His Tyr Thr Val Phe		
	355	360
Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu Val Phe Glu		
	370	375
Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys		
	385	390
Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser		
	405	410
Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe Lys His Arg His Pro		
	420	425
Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu		
	435	440
Ser Lys Ser Ser Ser Gln Leu Arg Met Ser Ser Leu Pro Ala Asp Asn		
	450	455
Leu Ala Thr		
465		

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

[illegible]

Met 1	His	Ser	Asp	Cys 5	Ile	Phe	Lys	Lys	Glu 10	Gln	Ala	Met	Cys	Leu 15	Glu
Arg	Ile	Gln	Arg 20	Ala	Asn	Asp	Leu	Met 25	Gly	Leu	Asn	Glu	Ser 30	Ser	Pro
Gly	Cys	Pro 35	Gly	Met	Trp	Asp	Asn 40	Ile	Thr	Cys	Trp	Lys 45	Pro	Ala	Gln
Val	Gly 50	Glu	Met	Val	Leu	Val 55	Ser	Cys	Pro	Glu	Val 60	Phe	Arg	Ile	Phe
Asn 65	Pro	Asp	Gln	Val	Trp 70	Met	Thr	Glu	Thr	Ile 75	Gly	Asp	Ser	Gly	Phe 80
Ala	Asp	Ser	Asn	Ser 85	Leu	Glu	Ile	Thr	Asp 90	Met	Gly	Val	Val	Gly 95	Arg
Asn	Cys	Thr	Glu 100	Asp	Gly	Trp	Ser	Glu 105	Pro	Phe	Pro	His	Tyr 110	Phe	Asp
Ala	Cys	Gly 115	Phe	Asp	Asp	Tyr	Glu 120	Pro	Glu	Ser	Gly	Asp 125	Gln	Asp	Tyr
Tyr 130	Tyr	Leu	Ser	Val	Lys	Ala 135	Leu	Tyr	Thr	Val	Gly 140	Tyr	Ser	Thr	Ser
Leu 145	Ala	Thr	Leu	Thr	Thr 150	Ala	Met	Val	Ile	Leu 155	Cys	Arg	Phe	Arg	Lys 160
Leu	His	Cys	Thr	Arg 165	Asn	Phe	Ile	His	Met 170	Asn	Leu	Phe	Val	Ser 175	Phe
Met	Leu	Arg	Ala 180	Ile	Ser	Val	Phe	Ile 185	Lys	Asp	Trp	Ile	Leu 190	Tyr	Ala
Glu	Gln	Asp 195	Ser	Ser	His	Cys	Phe 200	Val	Ser	Thr	Val	Glu 205	Cys	Lys	Ala
Val 210	Met	Val	Phe	Phe	His	Tyr 215	Cys	Val	Val	Ser	Asn 220	Tyr	Phe	Trp	Leu
Phe 225	Ile	Glu	Gly	Leu	Tyr 230	Leu	Phe	Thr	Leu	Leu 235	Val	Glu	Thr	Phe	Phe 240
Pro	Glu	Arg	Arg	Tyr 245	Phe	Tyr	Trp	Tyr	Thr 250	Ile	Ile	Gly	Trp	Gly 255	Thr
Pro	Thr	Val	Cys 260	Val	Thr	Val	Trp	Ala 265	Val	Leu	Arg	Leu	Tyr 270	Phe	Asp

Asp Ala Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val
 275 280 285
 Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe
 290 295 300
 Ile Gly Ile Ile Ile Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met
 305 310 315 320
 Gly Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr
 325 330 335
 Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu
 340 345 350
 Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro
 355 360 365
 Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val
 370 375 380
 Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln
 385 390 395 400
 Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln
 405 410 415
 Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe
 420 425 430
 Thr Met Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val
 435 440 445
 Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Leu
 450 455 460
 Arg Met Ser Ser Leu Pro Ala Asp Asn Leu Ala Thr
 465 470 475

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ala Arg Val Leu Gln Leu Ser Leu Thr Ala Leu Leu Leu Pro Val
1 5 10 15

Ala Ile Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met
20 25 30

Cys Leu Glu Arg Ile Gln Arg Ala Asn Asp Leu Met Gly Leu Asn Glu
35 40 45

Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys
50 55 60

Pro Ala Gln Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Val Phe
65 70 75 80

Arg Ile Phe Asn Pro Asp Gln Val Trp Met Thr Glu Thr Ile Gly Asp
85 90 95

Ser Gly Phe Ala Asp Ser Asn Ser Leu Glu Ile Thr Asp Met Gly Val
100 105 110

Val Gly Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His
115 120 125

Tyr Phe Asp Ala Cys Gly Phe Asp Asp Tyr Glu Pro Glu Ser Gly Asp
130 135 140

Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr
145 150 155 160

Ser Thr Ser Leu Ala Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg
165 170 175

Phe Arg Lys Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe
180 185 190

Val Ser Phe Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile
195 200 205

Leu Tyr Ala Glu Gln Asp Ser Ser His Cys Phe Val Ser Thr Val Glu
210 215 220

Cys Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr
225 230 235 240

Phe Trp Leu Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu
245 250 255

Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly
260 265 270

Trp Gly Thr Pro Thr Val Cys Val Thr Val Trp Ala Val Leu Arg Leu

275					280					285					
Tyr	Phe	Asp	Asp	Ala	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu
	290					295					300				
Trp	Trp	Val	Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe
305					310					315					320
Val	Leu	Phe	Ile	Gly	Ile	Ile	Ile	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser
				325					330					335	
Pro	Asp	Met	Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Ser	Cys	Val	Gln
			340					345					350		
Lys	Cys	Tyr	Cys	Lys	Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met
		355					360					365			
Ser	Glu	Leu	Ser	Thr	Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu
						375					380				
Leu	Ile	Pro	Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro
385					390					395					400
Glu	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	Gly
				405					410					415	
Ser	Phe	Gln	Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn	Gly
			420					425					430		
Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	Asn
		435					440					445			
Arg	Tyr	Phe	Thr	Met	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala	Ser
	450					455					460				
Ser	Gly	Val	Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser	Ser
465					470					475					480
Ser	Gln	Leu	Arg	Met	Ser	Ser	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr	
				485					490					495	

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu
1 5 10 15

Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His
35 40 45

Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe
50 55 60

Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe
65 70 75 80

Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg
85 90 95

Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp
100 105 110

Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr
115 120 125

Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser
130 135 140

Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys
145 150 155 160

Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe
165 170 175

Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala
180 185 190

Glu Gln Asp Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala
195 200 205

Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu
210 215 220

Phe Ile Glu Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe
225 230 235 240

Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr
245 250 255

Pro Thr Val Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe Asp
260 265 270

Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu	Trp	Trp	Val
		275					280					285			
Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe
	290					295					300				
Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met
305					310					315				320	
Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
				325					330					335	
Leu	Leu	Ile	Pro	Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser
			340					345					350		
Pro	Glu	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu
		355					360					365			
Gly	Ser	Phe	Gln	Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn
	370					375					380				
Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val
385					390					395				400	
Asn	Arg	Tyr	Phe	Ala	Val	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala
				405					410					415	
Ser	Ser	Gly	Val	Asn	Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser
			420					425					430		
Ser	Ser	Gln	Ile	Arg	Met	Ser	Gly	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr
		435					440					445			

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ala	Gly	Val	Val	His	Val	Ser	Leu	Ala	Ala	His	Cys	Gly	Ala	Cys
1				5					10					15	
Pro	Trp	Gly	Arg	Gly	Arg	Leu	Arg	Lys	Gly	Arg	Ala	Ala	Cys	Lys	Ser
			20					25					30		

Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu Leu Ser Val Gly
 35 40 45
 Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val
 50 55 60
 Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser
 65 70 75 80
 Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln
 85 90 95
 Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro
 100 105 110
 Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu
 115 120 125
 Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp
 130 135 140
 Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp Ser
 145 150 155 160
 Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr
 165 170 175
 Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly
 180 185 190
 Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu
 195 200 205
 Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr
 210 215 220
 Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys
 225 230 235 240
 Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg
 245 250 255
 Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp
 260 265 270
 Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val
 275 280 285
 Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu
 290 295 300
 Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg

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305 310 315 320
 Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val
 325 330 335
 Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe Asp Asp Thr Gly
 340 345 350
 Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile Lys Gly
 355 360 365
 Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile
 370 375 380
 Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn
 385 390 395 400
 Glu Ser Ser Ile Tyr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile
 405 410 415
 Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn
 420 425 430
 Val Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe
 435 440 445
 Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val
 450 455 460
 Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr
 465 470 475 480
 Phe Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly
 485 490 495
 Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser-Gln
 500 505 510
 Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr
 515 520 525

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

[illegible]

Met 1	His	Ser	Asp	Cys 5	Ile	Phe	Lys	Lys	Glu 10	Gln	Ala	Met	Cys	Leu 15	Glu
Lys	Ile	Gln	Arg 20	Ala	Asn	Glu	Leu	Met 25	Gly	Phe	Asn	Asp	Ser 30	Ser	Pro
Gly	Cys	Pro 35	Gly	Met	Trp	Asp	Asn 40	Ile	Thr	Cys	Trp	Lys 45	Pro	Ala	His
Val 50	Gly	Glu	Met	Val	Leu	Val 55	Ser	Cys	Pro	Glu	Leu 60	Phe	Arg	Ile	Phe
Asn 65	Pro	Asp	Gln	Val	Trp 70	Glu	Thr	Glu	Thr	Ile 75	Gly	Glu	Ser	Asp	Phe 80
Gly	Asp	Ser	Asn	Ser 85	Leu	Asp	Leu	Ser	Asp 90	Met	Gly	Val	Val	Ser 95	Arg
Asn	Cys	Thr	Glu 100	Asp	Gly	Trp	Ser	Glu 105	Pro	Phe	Pro	His	Tyr 110	Phe	Asp
Ala	Cys	Gly 115	Phe	Asp	Glu	Tyr	Glu 120	Ser	Glu	Thr	Gly	Asp 125	Gln	Asp	Tyr
Tyr 130	Tyr	Leu	Ser	Val	Lys	Ala 135	Leu	Tyr	Thr	Val	Gly 140	Tyr	Ser	Thr	Ser
Leu 145	Val	Thr	Leu	Thr	Thr 150	Ala	Met	Val	Ile	Leu 155	Cys	Arg	Phe	Arg	Lys 160
Leu	His	Cys	Thr	Arg 165	Asn	Phe	Ile	His	Met 170	Asn	Leu	Phe	Val	Ser 175	Phe
Met	Leu	Arg	Ala 180	Ile	Ser	Val	Phe	Ile 185	Lys	Asp	Trp	Ile	Leu 190	Tyr	Ala
Glu	Gln	Asp 195	Ser	Asn	His	Cys	Phe 200	Ile	Ser	Thr	Val	Glu 205	Cys	Lys	Ala
Val 210	Met	Val	Phe	Phe	His	Tyr 215	Cys	Val	Val	Ser	Asn 220	Tyr	Phe	Trp	Leu
Phe 225	Ile	Glu	Gly	Leu	Tyr 230	Leu	Phe	Thr	Leu	Leu 235	Val	Glu	Thr	Phe	Phe 240
Pro	Glu	Arg	Arg	Tyr 245	Phe	Tyr	Trp	Tyr	Thr 250	Ile	Ile	Gly	Trp	Gly 255	Thr
Pro	Thr	Val	Cys 260	Val	Thr	Val	Trp	Ala 265	Thr	Leu	Arg	Leu	Tyr 270	Phe	Asp

Asp Thr Gly Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val
 275 280 285
 Ile Lys Gly Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe
 290 295 300
 Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met
 305 310 315 320
 Gly Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr
 325 330 335
 Cys Lys Pro Gln Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu
 340 345 350
 Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro
 355 360 365
 Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val
 370 375 380
 Ser Lys Arg Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln
 385 390 395 400
 Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln
 405 410 415
 Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe
 420 425 430
 Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val
 435 440 445
 Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile
 450 455 460
 Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr
 465 470 475

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

176 -167-

Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys
1 5 10 15

Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser
20 25 30

Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu Leu Ser Val Gly
35 40 45

Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val
50 55 60

Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser
65 70 75 80

Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln
85 90 95

Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro
100 105 110

Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu
115 120 125

Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp
130 135 140

Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp Ser
145 150 155 160

Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg Asn Cys Thr
165 170 175

Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys Gly
180 185 190

Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu
195 200 205

Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr
210 215 220

Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys
225 230 235 240

Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg
245 250 255

Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp
260 265 270

Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val

176-167-176-167-176-167-

275					280					285					
Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu	Phe	Ile	Glu
290					295					300					
Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe	Pro	Glu	Arg
305					310					315					320
Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly	Trp	Gly	Thr	Pro	Thr	Val
				325					330					335	
Cys	Val	Thr	Val	Trp	Ala	Thr	Leu	Arg	Leu	Tyr	Phe	Asp	Asp	Thr	Gly
			340					345					350		
Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu	Trp	Trp	Val	Ile	Lys	Gly
		355					360					365			
Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe	Ile	Gly	Ile
						375					380				
Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met	Gly	Gly	Asn
385					390					395					400
Glu	Ser	Ser	Ile	Tyr	Phe	Ser	Cys	Val	Gln	Lys	Cys	Tyr	Cys	Lys	Pro
				405					410					415	
Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr	Ile
			420					425					430		
Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro	Leu	Phe	Gly
			435				440					445			
Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro	Glu	Asn	Val	Ser	Lys	Arg
	450				455					460					
Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	Gly	Ser	Phe	Gln	Gly	Phe	Val
465					470					475					480
Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile
			485						490					495	
Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	Asn	Arg	Tyr	Phe	Ala	Val	Asp
			500					505					510		
Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala	Ser	Ser	Gly	Val	Asn	Gly	Gly
		515					520					525			
Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser	Ser	Ser	Gln	Ile	Arg	Met	Ser
	530					535					540				
Gly	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr							
545					550										

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu
 1 5 10 15
 Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro
 20 25 30
 Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His
 35 40 45
 Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe
 50 55 60
 Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe
 65 70 75 80
 Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg
 85 90 95
 Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp
 100 105 110
 Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr
 115 120 125
 Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser
 130 135 140
 Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys
 145 150 155 160
 Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe
 165 170 175
 Met Leu Arg Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala
 180 185 190
 Glu Gln Asp Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala
 195 200 205

119-170-

Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu
210						215					220				
Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe
225					230					235					240
Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly	Trp	Gly	Thr
				245					250					255	
Pro	Thr	Val	Cys	Val	Thr	Val	Trp	Ala	Thr	Leu	Arg	Leu	Tyr	Phe	Asp
			260					265					270		
Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu	Trp	Trp	Val
		275					280					285			
Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe
	290					295					300				
Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met
305					310					315					320
Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Cys	Val	Gln	Lys	Cys	Tyr	Cys
				325					330					335	
Lys	Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser
			340					345					350		
Thr	Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro	Leu
		355					360					365			
Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro	Glu	Asn	Val	Ser
	370					375					380				
Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	Gly	Ser	Phe	Gln	Gly
385					390					395					400
Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn	Gly	Glu	Val	Gln	Ala
				405					410					415	
Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	Asn	Arg	Tyr	Phe	Ala
			420					425					430		
Val	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala	Ser	Ser	Gly	Val	Asn
		435					440					445			
Gly	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser	Ser	Ser	Gln	Ile	Arg
	450					455					460				
Met	Ser	Gly	Leu	Pro	Ala	Asp	Asn	Leu	Ala	Thr					
465					470					475					

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 552 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser Leu Val Thr
210 215 220

Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys Leu His Cys
225 230 235 240

Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg
245 250 255

Ala Ile Ser Val Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp
260 265 270

Ser Asn His Cys Phe Ile Ser Thr Val Glu Cys Lys Ala Val Met Val
275 280 285

Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu
290 295 300

Gly Leu Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg
305 310 315 320

Arg Tyr Phe Tyr Trp Tyr Thr Ile Ile Gly Trp Gly Thr Pro Thr Val
325 330 335

Cys Val Thr Val Trp Ala Thr Leu Arg Leu Tyr Phe Asp Asp Thr Gly
340 345 350

Cys Trp Asp Met Asn Asp Ser Thr Ala Leu Trp Trp Val Ile Lys Gly
355 360 365

Pro Val Val Gly Ser Ile Met Val Asn Phe Val Leu Phe Ile Gly Ile
370 375 380

Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly Gly Asn
385 390 395 400

Glu Ser Ser Ile Tyr Phe Cys Val Gln Lys Cys Tyr Cys Lys Pro Gln
405 410 415

Arg Ala Gln Gln His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr
420 425 430

Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile
435 440 445

His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu
450 455 460

Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val
465 470 475 480

Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile Lys
485 490 495

Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Ala Val Asp Phe

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182-173-

500

505

510

Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr
515 520 525

Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser Gly
530 535 540

Leu Pro Ala Asp Asn Leu Ala Thr
545 550

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 476 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu
1 5 10 15

Lys Ile Gln Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro
20 25 30

Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His
35 40 45

Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe
50 55 60

Asn Pro Asp Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe
65 70 75 80

Gly Asp Ser Asn Ser Leu Asp Leu Ser Asp Met Gly Val Val Ser Arg
85 90 95

Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp
100 105 110

Ala Cys Gly Phe Asp Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr
115 120 125

Tyr Tyr Leu Ser Val Lys Ala Leu Tyr Thr Val Gly Tyr Ser Thr Ser
130 135 140

Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys

145					150					155				160
Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser
				165					170					175
Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr
			180					185					190	Ala
Glu	Gln	Asp	Ser	Asn	His	Cys	Phe	Ile	Ser	Thr	Val	Glu	Cys	Lys
		195					200					205		Ala
Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp
	210					215					220			Leu
Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe
225					230					235				240
Pro	Glu	Arg	Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly	Trp	Gly
				245					250					255
Pro	Thr	Val	Cys	Val	Thr	Val	Trp	Ala	Thr	Leu	Arg	Leu	Tyr	Phe
			260					265					270	Asp
Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu	Trp	Trp
		275					280					285		Val
Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu
	290					295					300			Phe
Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp
305					310					315				Met
Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Leu	Thr	Asn	Leu	Ser	Pro	Arg
				325					330					335
Pro	Lys	Lys	Ala	Arg	Glu	Asp	Pro	Leu	Pro	Val	Pro	Ser	Asp	Gln
			340					345					350	His
Ser	Leu	Pro	Phe	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile
		355					360					365		Pro
Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro	Glu	Asn
	370					375					380			Val
Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	Gly	Ser	Phe
385					390					395				Gln
Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn	Gly	Glu	Val
				405					410					415
Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	Asn	Arg	Tyr
			420					425					430	Phe

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Ala Val Asp Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val
435 440 445

Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile
450 455 460

Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr
465 470 475

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ala Gly Val Val His Val Ser Leu Ala Ala His Cys Gly Ala Cys
1 5 10 15

Pro Trp Gly Arg Gly Arg Leu Arg Lys Gly Arg Ala Ala Cys Lys Ser
20 25 30

Ala Ala Gln Arg His Ile Gly Ala Asp Leu Pro Leu Leu Ser Val Gly
35 40 45

Gly Gln Trp Cys Trp Pro Arg Ser Val Met Ala Gly Val Val His Val
50 55 60

Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Pro Ala Met His Ser
65 70 75 80

Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln
85 90 95

Arg Ala Asn Glu Leu Met Gly Phe Asn Asp Ser Ser Pro Gly Cys Pro
100 105 110

Gly Met Trp Asp Asn Ile Thr Cys Trp Lys Pro Ala His Val Gly Glu
115 120 125

Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp
130 135 140

Gln Val Trp Glu Thr Glu Thr Ile Gly Glu Ser Asp Phe Gly Asp Ser
145 150 155 160

[illegible]

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Asn	Ser	Leu	Asp	Leu	Ser	Asp	Met	Gly	Val	Val	Ser	Arg	Asn	Cys	Thr
				165					170					175	
Glu	Asp	Gly	Trp	Ser	Glu	Pro	Phe	Pro	His	Tyr	Phe	Asp	Ala	Cys	Gly
			180					185					190		
Phe	Asp	Glu	Tyr	Glu	Ser	Glu	Thr	Gly	Asp	Gln	Asp	Tyr	Tyr	Tyr	Leu
		195					200					205			
Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	Leu	Val	Thr
	210					215					220				
Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	Leu	His	Cys
225					230					235					240
Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg
				245					250					255	
Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	Glu	Gln	Asp
			260					265					270		
Ser	Asn	His	Cys	Phe	Ile	Ser	Thr	Val	Glu	Cys	Lys	Ala	Val	Met	Val
		275					280					285			
Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu	Phe	Ile	Glu
	290					295					300				
Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe	Pro	Glu	Arg
305					310					315					320
Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly	Trp	Gly	Thr	Pro	Thr	Val
				325					330					335	
Cys	Val	Thr	Val	Trp	Ala	Thr	Leu	Arg	Leu	Tyr	Phe	Asp	Asp	Thr	Gly
			340					345					350		
Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu	Trp	Trp	Val	Ile	Lys	Gly
		355					360					365			
Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe	Ile	Gly	Ile
	370					375					380				
Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met	Gly	Gly	Asn
385					390					395					400
Glu	Ser	Ser	Ile	Tyr	Leu	Thr	Asn	Leu	Ser	Pro	Arg	Val	Pro	Lys	Lys
				405					410					415	
Ala	Arg	Glu	Asp	Pro	Leu	Pro	Val	Pro	Ser	Asp	Gln	His	Ser	Leu	Pro
			420					425					430		
Phe	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro	Leu	Phe	Gly

435		440		445
Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg				
450		455		460
Glu Arg Leu Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val				
465		470		480
Val Ala Val Leu Tyr Cys Phe Leu Asn Gly Glu Val Gln Ala Glu Ile				
	485		490	495
Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Ala Val Asp				
	500		505	510
Phe Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly				
	515		520	525
Thr Gln Leu Ser Ile Leu Ser Lys Ser Ser Ser Gln Ile Arg Met Ser				
	530		535	540
Gly Leu Pro Ala Asp Asn Leu Ala Thr				
545		550		

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGAGAGGCG GGCGGCACTG GCCCGAGCCG CCTTGCAGGC TGAGAAGCGT CATGGCCAGC	60
ATCGCGCAGG TCTCCCTGGC TGCTCTCCTC CTGCTGCCTA TGGCCACCGC CATGCATTCC	120
GACTGCATCT TCAAGAAGGA GCAAGCCATG TGCCTGGAGA AGATCCAGAG GGTGAATGAC	180
CTGATGGGCT TGAATGACTC CTCCCCAGGG TGCCCTGGGA TGTGGGACAA CATCACGTGT	240
TGGAAGCCCG CCCACGTGGG TGAGATGGTC CTGGTCAGTT GCCCTGAACT CTTCCGAATC	300
TTCAACCCAG ACCAAGTCTG GGAGACGGAA ACCATCGGAG AGTTCGGTTT TGCAGACAGT	360

AAATCCTTGG ATCTCTCAGA CATGAGGGTG GTGAGCCGGA ATTGCACGGA GGATGGATGG	420
TCAGAGCCAT TCCCTCATTA TTTCGATGCC TGTGGGTTTG AGGAGTACGA ATCTGAGACT	480
GGGGACCAGG ATTACTACTA CCTGTCAGTG AAGGCCCTGT ACACAGTTGG CTACAGCACG	540
TCCCTCGTCA CCCTCACCAC TGCCATGGTC ATCCTGTGTC GTTTCGGAA GCTGCACTGC	600
ACCCGCAACT TCATCCACAT GAACCTCTTC GTGTCGTTTA TGCTGAGGGC CATCTCCGTC	660
TTCATCAAAG ACTGGATCCT CTATGCTGAG CAGGACAGCA ATCACTGCTT TGTCTCCACT	720
GTGGAATGCA AGGCTGTGAT GGTTTTCTTC CACTACTGTG TTGTATCCAA CTACTTCTGG	780
CTGTTTCATCG AGGGCCTGTA TCTCTTCACC CTGCTGGTGG AGACCTTCTT CCCCAGAGAGG	840
AGATAATTCT ACTGGTACAT CATCATTGGC TGGGGGACAC CAACTGTGTG TGTGTCTGTG	900
TGGGCTATGC TGAGGCTCTA CTTCGATGAC ACAGGCTGCT GGGATATGAA TGACAACACG	960
GCTCTGTGGT GGGTGATCAA AGGCCCTGTA GTTGGCTCCA TAATGGTTAA TTTTGTGCTC	1020
TTCATCGGCA TCATTGTCAT CCTTGTGCAG AAACCTTCAGT CTCCAGACAT GGGAGGCAAC	1080
GAGTCCAGCA TCTACTTCAG CTGCGTGCAG AAATGCTACT GCAAGCCACA GCGGGCTCAG	1140
CAGCACTCTT GCAAGATGTC AGAACTGTCC ACCATTACTC TACGGCTCGC CAGGTCCACC	1200
TTGCTGCTCA TCCCACTCTT TGGAATCCAC TACACTGTCT TTGCTTTCTC CCCGGAGAAC	1260
GTGAGCAAGA GGGAGAGACT GGTGTTTGAG CTGGGTCTGG GCTCCTTCCA GGGCTTTGTG	1320
GTGGCTGTTT TCTATTGCTT TCTGAATGGA GAGGTGCAGG CGGAGATCAA GAGGAAGTGG	1380
CGGAGCTGGA AGGTGAACCG CTACTTCACC ATGGACTTCA AGCACC GGCA CCCATCCCTG	1440
GCCAGCAGCG GGGTGAACCG GGGCACCCAG CTCTCCATCC TGAGCAAGAG CAGCTCCCAG	1500
ATCCGCATGT CTGGGCTTCC GGCCGACAAC CTGGCCACC	1539

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..1455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGAGAGGCG GCGGGCACTG GCCCGAGCCG CCTTGCAGGC TGAGAAGCGT CATGGCCAGC	60
ATCGCGCAGG TCTCCCTGGC TGCTCTCCTC CTGCTGCCTA TGGCCACCGC CATGCATTCC	120
GACTGCATCT TCAAGAAGGA GCAAGCCATG TGCCTGGAGA AGATCCAGAG GGTGAATGAC	180
CTGATGGGCT TGAATGACTC CTCCCCAGGG TGCCCTGGGA TGTGGGACAA CATCACGTGT	240
TGGAAGCCCG CCCACGTGGG TGAGATGGTC CTGGTCAGTT GCCCTGAACT CTTCCGAATC	300
TTCAACCCAG ACCAAGTCTG GGAGACGGAA ACCATCGGAG AGTTCGGTTT TGCAGACAGT	360
AAATCCTTGG ATCTCTCAGA CATGAGGGTG GTGAGCCGGA ATTGCACGGA GGATGGATGG	420
TCAGAGCCAT TCCCTCATTA TTTCGATGCC TGTGGGTTTG AGGAGTACGA ATCTGAGACT	480
GGGGAACCAGG ATTACTACTA CCTGTCAGTG AAGGCCCTGT ACACAGTTGG CTACAGCACG	540
TCCTCGTCA CCCTCACCAC TGCCATGGTC ATCCTGTGTC GTTTCGGAA GCTGCACTGC	600
ACCGCAACT TCATCCACAT GAACCTCTTC GTGTCGTTTA TGCTGAGGGC CATCTCCGTC	660
TTGATCAAAG ACTGGATCCT CTATGCTGAG CAGGACAGCA ATCACTGCTT TGTCTCCACT	720
GTGGAATGCA AGGCTGTGAT GGTTTTCTTC CACTACTGTG TTGTATCCAA CTACTTCTGG	780
CTGTTTCATCG AGGGCCTGTA TCTCTTCACC CTGCTGGTGG AGACCTTCTT CCCCAGAGAG	840
AGATATTTCT ACTGGTACAT CATCATTGGC TGGGGGACAC CAACTGTGTG TGTGTCTGTG	900
TGGGCTATGC TGAGGCTCTA CTTGATGAC ACAGGCTGCT GGGATATGAA TGACAACACG	960
GCTCTGTGGT GGGTGATCAA AGGCCCTGTA GTTGGCTCCA TAATGGTTAA TTTTGTGCTC	1020
TTCATCGGCA TCATTGTCAT CCTTGTGCAG AAACCTCAGT CTCCAGACAT GGGAGGCAAC	1080
GAGTCCAGCA TCTACTTACG GCTCGCCAGG TCCACCTTGC TGCTCATCCC ACTCTTTGGA	1140
ATCCACTACA CTGTCTTTGC TTTCTCCCCG GAGAACGTCA GCAAGAGGGA GAGACTGGTG	1200
TTTGAGCTGG GTCTGGGCTC CTTCCAGGGC TTTGTGGTGG CTGTTCTCTA TTGCTTTCTG	1260
AATGGAGAGG TGCAGGCGGA GATCAAGAGG AAGTGGCGGA GCTGGAAGGT GAACCGCTAC	1320
TTCACCATGG ACTTCAAGCA CCGGCACCCA TCCCTGGCCA GCAGCGGGGT GAACGGGGGC	1380

ACCCAGCTCT CCATCCTGAG CAAGAGCAGC TCCCAGATCC GCATGTCTGG GCTTCCGGCC 1440
 GACAACCTGG CCACC 1455

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATGCCAGAG TCCTGCAGCT CTCCCTGACT GCTCTCCTGC TGCCTGTGGC TATTGCTATG 60
 CACTCTGACT GCATCTTCAA GAAGGAGCAA GCCATGTGCC TGGAGAGGAT CCAGAGGGCC 120
 AAGGACCTGA TGGGACTAAA CGAGTCTTCC CCAGGTTGCC CTGGCATGTG GGACAATATC 180
 ACATGTTGGA AGCCAGCTCA AGTAGGTGAG ATGGTCCTTG TAAGCTGCCC TGAGGTCTTC 240
 CGGATCTTCA ACCCGGACCA AGTCTGGATG ACAGAAACCA TAGGAGATTC TGGTTTTGCC 300
 GATAGTAATT CCTTGGAGAT CACAGACATG GGGGTCGTGG GCCGGAAGCTG CACAGAGGAC 360
 GGCTGGTCCG AGCCCTTCCC CCACTACTTC GATGCTTGTT GGTTTGATGA TTATGAGCCT 420
 GAGTCTGGAG ATCAGGATTA TTACTACCTG TCGGTGAAGG CTCTCTACAC AGTCGGCTAC 480
 AGCACTTCCC TCGCCACCCT CACTACTGCC ATGGTCATCT TGTGCCGCTT CCGGAAGCTG 540
 CATTGCACTC GCAACTTCAT CCACATGAAC CTGTTTGTAT CCTTCATGCT GAGGGCTATC 600
 TCCGTCTTCA TCAAGGACTG GATCTTGTAC GCCGAGCAGG ACAGCAGTCA CTGCTTCGTT 660
 TCCACCGTGG AGTGCAAAGC TGTCATGGTT TTCTTCCACT ACTGCGTGGT GTCCAACCTAC 720
 TTCTGGCTGT TCATTGAAGG CCTGTACCTC TTTACACTGC TGGTGGAGAC CTTCTTCCCT 780
 GAGAGGAGAT ATTTCTACTG GTACACCATC ATCGGCTGGG GGACACCTAC TGTGTGTGTA 840
 ACAGTGTGGG CTGTGCTGAG GCTCTATTTT GATGATGCAG GATGCTGGGA TATGAATGAC 900

AGCACAGCTC TGTGGTGGGT GATCAAAGGC CCCGTGGTTG GCTCTATAAT GGTAACTTT 960
 GTGCTTTTCA TCGGCATCAT CATCATCCTT GTACAGAAGC TGCAGTCCCC AGACATGGGA 1020
 GGCAACGAGT CCAGCATCTA CTTACGGCTG GCCCGCTCCA CCCTACTGCT CATCCCACTC 1080
 TTCGGAATCC ACTACACAGT ATTCGCCTTC TCTCCAGAGA ACGTCAGCAA GAGGGAAAGA 1140
 CTTGTGTTTG AGCTTGGGCT GGGCTCCTTC CAGGGCTTTG TGGTGGCTGT ACTCTACTGC 1200
 TTCCTGAATG GGGAGGTACA GGCAGAGATT AAGAGGAAAT GGAGGAGCTG GAAGGTGAAC 1260
 CGTTACTTCA CTATGGACTT CAAGCACCGG CACCCGTCCC TGGCCAGCAG TGGAGTAAAT 1320
 GGGGGAACCC AGCTGTCCAT CCTGAGCAAG AGCAGCTCCC AGCTCCGCAT GTCCAGCCTC 1380
 CCGGCCGACA ACTTGGCCAC C 1401

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGGCCAGAG TCCTGCAGCT CTCCCTGACT GCTCTCCTGC TGCCTGTGGC TATTGCTATG 60
 CACTCTGACT GCATCTTCAA GAAGGAGCAA GCCATGTGCC TGGAGAGGAT CCAGAGGGCC 120
 AACGACCTGA TGGGACTAAA CGAGTCTTCC CCAGGTTGCC CTGGCATGTG GGACAATATC 180
 ACATGTTGGA AGCCAGCTCA AGTAGGTGAG ATGGTCCTTG TAAGCTGCCC TGAGGTCTTC 240
 CGGATCTTCA ACCCGGACCA AGTCTGGATG ACAGAAACCA TAGGAGATTC TGGTTTTGCC 300
 GATAGTAATT CCTTGGAGAT CACAGACATG GGGGTCGTGG GCCGGAAGTG CACAGAGGAC 360
 GGCTGGTCGG AGCCCTTCCC CCACTACTTC GATGCTTGTG GGTTTGATGA TTATGAGCCT 420
 GAGTCTGGAG ATCAGGATTA TTACTACCTG TCGGTGAAGG CTCTCTACAC AGTCGGCTAC 480

AGCACTTCCC	TCGCCACCCT	CACTACTGCC	ATGGTCATCT	TGTGCCGCTT	CCGGAAGCTG	540
CATTGCACTC	GCAACTTCAT	CCACATGAAC	CTGTTTGTAT	CCTTCATGCT	GAGGGCTATC	600
TCCGTCTTCA	TCAAGGACTG	GATCTTGTA	GCCGAGCAGG	ACAGCAGTCA	CTGCTTCGTT	660
TCCACCGTGG	AGTGCAAAGC	TGTCATGGTT	TTCTTCCACT	ACTGCGTGGT	GTCCAACTAC	720
TTCTGGCTGT	TCATTGAAGG	CCTGTACCTC	TTTACACTGC	TGGTGGAGAC	CTTCTTCCCT	780
GAGAGGAGAT	ATTTCTACTG	GTACACCATC	ATCGGCTGGG	GGACACCTAC	TGTGTGTGTA	840
ACAGTGTGGG	CTGTGCTGAG	GCTCTATTTT	GATGATGCAG	GATGCTGGGA	TATGAATGAC	900
AGCACAGCTC	TGTGGTGGGT	GATCAAAGGC	CCCGTGTTG	GCTCTATAAT	GGTAACTTT	960
GTGCTTTTCA	TCGGCATCAT	CATCATCCTT	GTACAGAAGC	TGCAGTCCCC	AGACATGGGA	1020
GGCAACGAGT	CCAGCATCTA	CTTCAGCTGC	GTGCAGAAAT	GCTACTGCAA	GCCACAGCGG	1080
GCTCAGCAGC	ACTCTTGCAA	GATGTCAGAA	CTATCCACCA	TTACTCTACG	GCTGGCCCCG	1140
TCCACCCTAC	TGCTCATCCC	ACTCTTCGGA	ATCCACTACA	CAGTATTTCG	CTTCTCTCCA	1200
GAGAACGTCA	GCAAGAGGGA	AAGACTTGTG	TTTGAGCTTG	GGCTGGGCTC	CTTCCAGGGC	1260
TTTGTGGTGG	CTGTACTCTA	CTGCTTCCTG	AATGGGGAGG	TACAGGCAGA	GATTAAGAGG	1320
AAATGGAGGA	GCTGGAAGGT	GAACCGTTAC	TTCACTATGG	ACTTCAAGCA	CCGGCACCCG	1380
TCCCTGGCCA	GCAGTGGAGT	AAATGGGGGA	ACCCAGCTGT	CCATCCTGAG	CAAGAGCAGC	1440
TCCCAGCTCC	GCATGTCCAG	CCTCCCGGCC	GACAACTTGG	CCACC		1485

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ATGGCTGGTG	TCGTGCACGT	TTCCCTGGCT	GCTCACTGCG	GGGCCTGTCC	GTGGGGCCGG	60
GGCAGACTCC	GCAAAGGACG	CGCAGCCTGC	AAGTCCGCGG	CCCAGAGACA	CATTGGGGCT	120
GACCTGCCGC	TGCTGTCAGT	GGGAGGCCAG	TGGTGCTGGC	CAAGAAGTGT	CATGGCTGGT	180
GTCGTGCACG	TTTCCCTGGC	TGCTCTCCTC	CTGCTGCCTA	TGGCCCCTGC	CATGCATTCT	240
GACTGCATCT	TCAAGAAGGA	GCAAGCCATG	TGCCTGGAGA	AGATCCAGAG	GGCCAATGAG	300
CTGATGGGCT	TCAATGATTG	CTCTCCAGGC	TGTCCTGGGA	TGTGGGACAA	CATCACGTGT	360
TGGAAGCCCG	CCCATGTGGG	TGAGATGGTC	CTGGTCAGCT	GCCCTGAGCT	CTTCCGAATC	420
TTCAACCCAG	ACCAAGTCTG	GGAGACCGAA	ACCATTGGAG	AGTCTGATTT	TGGTGACAGT	480
AACTCCTTAG	ATCTCTCAGA	CATGGGAGTG	GTGAGCCGGA	ACTGCACGGA	GGATGGCTGG	540
TCGGAACCCT	TCCCTCATTG	CTTTGATGCC	TGTGGGTTTG	ATGAATATGA	ATCTGAGACT	600
GGGGACCAGG	ATTATTACTA	CCTGTCAGTG	AAGGCCCTCT	ACACGGTTGG	CTACAGCACA	660
TGCTCTCGTCA	CCCTCACCAC	TGCCATGGTC	ATCCTTTGTC	GCTTCCGGAA	GCTGCACTGC	720
ACACGCAACT	TCATCCACAT	GAACCTGTTT	GTGTCGTTCA	TGCTGAGGGC	GATCTCCGTC	780
TTTCATCAAAG	ACTGGATTCT	GTATGCGGAG	CAGGACAGCA	ACCACTGCTT	CATCTCCACT	840
GTGGAATGTA	AGGCCGTCAT	GGTTTTCTTC	CACTACTGTG	TTGTGTCCAA	CTACTTCTGG	900
CTGTTCATCG	AGGGCCTGTA	CCTCTTCACT	CTGCTGGTGG	AGACCTTCTT	CCCTGAAAGG	960
AGATACTTCT	ACTGGTACAC	CATCATTTGGC	TGGGGGTCCC	CAACTGTGTG	TGTGACAGTG	1020
TGGGCTACGC	TGAGACTCTA	CTTTGATGAC	ACAGGCTGCT	GGGATATGAA	TGACAGCACA	1080
GCTCTGTGGT	GGGTGATCAA	AGGCCCTGTG	GTTGGCTCTA	TCATGGTTAA	CTTTGTGCTT	1140
TTTATTGGCA	TTATCGTCAT	CCTTGTGCAG	AAACTTCAGT	CTCCAGACAT	GGGAGGCAAT	1200
GAGTCCAGCA	TCTACTTGCG	ACTGGCCCGG	TCCACCCTGC	TGCTCATCCC	ACTATTCGGA	1260
ATCCACTACA	CAGTATTTGC	CTTCTCCCCA	GAGAATGTCA	GCAAAAGGGA	AAGACTCGTG	1320
TTTGAGCTGG	GGCTGGGCTC	CTTCCAGGGC	TTTGTGGTGG	CTGTTCTCTA	CTGTTTTCTG	1380
AATGGTGAGG	TACAAGCGGA	GATCAAGCGA	AAATGGCGAA	GCTGGAAGGT	GAACCGTTAC	1440
TTCGCTGTGG	ACTTCAAGCA	CCGACACCCG	TCTCTGGCCA	GCAGTGGGGT	GAATGGGGGC	1500
ACCCAGCTCT	CCATCCTGAG	CAAGAGCAGC	TCCCAAATCC	GCATGTCTGG	CCTCCCTGCT	1560

GACAATCTGG CCACC

1575

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGGCTGGTG TCGTGCACGT TTCCCTGGCT GCTCACTGCG GGGCCTGTCC GTGGGGCCGG	60
GGCAGACTCC GCAAAGGACG CGCAGCCTGC AAGTCCGCGG CCCAGAGACA CATTTGGGGCT	120
GAGCTGCCGC TGCTGTCAGT GGGAGGCCAG TGGTGCTGGC CAAGAAGTGT CATGGCTGGT	180
GTGGTGACAG TTTCCCTGGC TGCTCTCCTC CTGCTGCCTA TGGCCCCTGC CATGCATTCT	240
GAGTGCATCT TCAAGAAGGA GCAAGCCATG TGCCTGGAGA AGATCCAGAG GGCCAATGAG	300
CTGATGGGCT TCAATGATTC CTCTCCAGGC TGTCCTGGGA TGTGGGACAA CATCACGTGT	360
TGGAAGCCCG CCCATGTGGG TGAGATGGTC CTGGTCAGCT GCCCTGAGCT CTTCCGAATC	420
TTCAACCCAG ACCAAGTCTG GGAGACCGAA ACCATTGGAG AGTCTGATTT TGGTGACAGT	480
AACTCCTTAG ATCTCTCAGA CATGGGAGTG GTGAGCCGGA ACTGCACGGA GGATGGCTGG	540
TCGGAACCCT TCCCTCATT CTTTGATGCC TGTGGGTTTG ATGAATATGA ATCTGAGACT	600
GGGGACCAGG ATTATTACTA CCTGTCAGTG AAGGCCCTCT ACACGGTTGG CTACAGCACA	660
TCCCTCGTCA CCCTCACCAC TGCCATGGTC ATCCTTTGTC GCTTCCGGAA GCTGCACTGC	720
ACACGCAACT TCATCCACAT GAACCTGTTT GTGTCGTTCA TGCTGAGGGC GATCTCCGTC	780
TTCATCAAAG ACTGGATTCT GTATGCGGAG CAGGACAGCA ACCACTGCTT CATCTCCACT	840
GTGGAATGTA AGGCCGTCAT GGTTCCTTTC CACTACTGTG TTGTGTCCAA CTACTTCTGG	900
CTGTTTCATCG AGGGCCTGTA CCTCTTCACT CTGCTGGTGG AGACCTTCTT CCCTGAAAGG	960

AGATACTTCT ACTGGTACAC CATCATTGGC TGGGGGACCC CAACTGTGTG TGTGACAGTG 1020
 TGGGCTACGC TGAGACTCTA CTTTGATGAC ACAGGCTGCT GGGATATGAA TGACAGCACA 1080
 GCTCTGTGGT GGGTGATCAA AGGCCCTGTG GTTGGCTCTA TCATGGTTAA CTTTGTGCTT 1140
 TTTATTGGCA TTATCGTCAT CCTTGTGCAG AAACCTCAGT CTCCAGACAT GGGAGGCAAT 1200
 GAGTCCAGCA TCTACTTCAG CTGCGTGCAG AAATGCTACT GCAAGCCACA GCGGGCTCAG 1260
 CAGCACTCTT GCAAGATGTC AGAACTGTCC ACCATTACTC TGCGACTGGC CCGGTCCACC 1320
 CTGCTGCTCA TCCCACTATT CGGAATCCAC TACACAGTAT TTGCCTTCTC CCCAGAGAAT 1380
 GTCAGCAAAA GGGAAAGACT CGTGTTTGAG CTGGGGCTGG GCTCCTTCCA GGGCTTTGTG 1440
 GTGGCTGTTT TCTACTGTTT TCTGAATGGT GAGGTACAAG CGGAGATCAA GCGAAAATGG 1500
 CGAAGCTGGA AGGTGAACCG TTA CTTCGCT GTGGACTTCA AGCACCGACA CCCGTCTCTG 1560
 GCCAGCAGTG GGGTGAATGG GGGCACCCAG CTCTCCATCC TGAGCAAGAG CAGCTCCCAA 1620
 ATCGCATGT CTGGCCTCCC TGCTGACAAT CTGGCCACC 1659

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..1656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATGGCTGGTG TCGTGACAGT TTCCCTGGCT GCTCACTGCG GGGCCTGTCC GTGGGGCCGG 60
 GGCAGACTCC GCAAAGGACG CGCAGCCTGC AAGTCCGCGG CCCAGAGACA CATTGGGGCT 120
 GACCTGCCGC TGCTGTCAGT GGGAGGCCAG TGGTGCTGGC CAAGAAGTGT CATGGCTGGT 180
 GTCGTGCACG TTTCCCTGGC TGCTCTCCTC CTGCTGCCTA TGGCCCCTGC CATGCATTCT 240
 GACTGCATCT TCAAGAAGGA GCAAGCCATG TGCCTGGAGA AGATCCAGAG GGCCAATGAG 300

CTGATGGGCT TCAATGATTC CTCTCCAGGC TGTCTGGGA TGTGGGACAA CATCACGTGT	360
TGGAAGCCCG CCCATGTGGG TGAGATGGTC CTGGTCAGCT GCCCTGAGCT CTTCCGAATC	420
TTCAACCCAG ACCAAGTCTG GGAGACCGAA ACCATTGGAG AGTCTGATTT TGGTGACAGT	480
AACTCCTTAG ATCTCTCAGA CATGGGAGTG GTGAGCCGGA ACTGCACGGA GGATGGCTGG	540
TCGGAACCCT TCCCTCATTA CTTTGATGCC TGTGGGTTTG ATGAATATGA ATCTGAGACT	600
GGGGACCAGG ATTATTACTA CCTGTCAGTG AAGGCCCTCT ACACGGTTGG CTACAGCACA	660
TCCCTCGTCA CCCTCACCAC TGCCATGGTC ATCCTTTGTC GCTTCCGGAA GCTGCACTGC	720
ACACGCAACT TCATCCACAT GAACCTGTTT GTGTCGTTCA TGCTGAGGGC GATCTCCGTC	780
TTCAATCAAAG ACTGGATTCT GTATGCGGAG CAGGACAGCA ACCACTGCTT CATCTCCACT	840
GTGGAATGTA AGGCCGTCAT GGTTTTCTTC CACTACTGTG TTGTGTCCAA CTACTTCTGG	900
CTGTTTCATCG AGGGCCTGTA CCTCTTCACT CTGCTGGTGG AGACCTTCTT CCCTGAAAGG	960
AGATACTTCT ACTGGTACAC CATCATTTGGC TGGGGGACCC CAACTGTGTG TGTGACAGTG	1020
TGGGCTACGC TGAGACTCTA CTTTGATGAC ACAGGCTGCT GGGATATGAA TGACAGCACA	1080
GCTGTGTGGT GGGTGATCAA AGGCCCTGTG GTTGGCTCTA TCATGGTTAA CTTTGTGCTT	1140
TTTATTGGCA TTATCGTCAT CCTTGTGCAG AAACCTCAGT CTCCAGACAT GGGAGGCAAT	1200
GAGTCCAGCA TCTACTTCTG CGTGCAGAAA TGCTACTGCA AGCCACAGCG GGCTCAGCAG	1260
CACTCTTGCA AGATGTCAGA ACTGTCCACC ATTACTCTGC GACTGGCCCG GTCCACCCTG	1320
CTGCTCATCC CACTATTCTG AATCCACTAC ACAGTATTTG CCTTCTCCCC AGAGAATGTC	1380
AGCAAAAGGG AAAGACTCGT GTTTGAGCTG GGGCTGGGCT CCTTCCAGGG CTTTGTGGTG	1440
GCTGTTCTCT ACTGTTTTCT GAATGGTGAG GTACAAGCGG AGATCAAGCG AAAATGGCGA	1500
AGCTGGAAGG TGAACCGTTA CTTGCTGTG GACTTCAAGC ACCGACACCC GTCTCTGGCC	1560
AGCAGTGGGG TGAATGGGGG CACCCAGCTC TCCATCCTGA GCAAGAGCAG CTCCCAAATC	1620
CGCATGTCTG GCCTCCCTGC TGACAATCTG GCCACC	1656

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1659 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..1659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATGGCTGGTG TCGTGACAGT TTCCCTGGCT GCTCACTGCG GGGCCTGTCC GTGGGGCCGG	60
GGCAGACTCC GCAAAGGACG CGCAGCCTGC AAGTCCGCGG CCCAGAGACA CATTGGGGCT	120
GACCTGCCGC TGCTGTCAGT GGGAGGCCAG TGGTGCTGGC CAAGAAGTGT CATGGCTGGT	180
GTGGTGCACG TTTCCCTGGC TGCTCTCCTC CTGCTGCCTA TGGCCCCTGC CATGCATTCT	240
GACGTGCATCT TCAAGAAGGA GCAAGCCATG TGCCTGGAGA AGATCCAGAG GGCCAATGAG	300
CTGATGGGCT TCAATGATTC CTCTCCAGGC TGTCCTGGGA TGTGGGACAA CATCACGTGT	360
TGGAAGCCCG CCCATGTGGG TGAGATGGTC CTGGTCAGCT GCCCTGAGCT CTTCCGAATC	420
TTCAACCCAG ACCAAGTCTG GGAGACCGAA ACCATTGGAG AGTCTGATTT TGGTGACAGT	480
AACTCCTTAG ATCTCTCAGA CATGGGAGTG GTGAGCCGGA ACTGCACGGA GGATGGCTGG	540
TGGGAACCCT TCCCTCATTA CTTTGATGCC TGTGGGTTTG ATGAATATGA ATCTGAGACT	600
GGGGACCAGG ATTATTACTA CCTGTCAGTG AAGGCCCTCT ACACGGTTGG CTACAGCACA	660
TCCCTCGTCA CCCTCACCAC TGCCATGGTC ATCCTTTGTC GCTTCCGGAA GCTGCACTGC	720
ACACGCAACT TCATCCACAT GAACCTGTTT GTGTCGTTCA TGCTGAGGGC GATCTCCGTC	780
TTCATCAAAG ACTGGATTCT GTATGCGGAG CAGGACAGCA ACCACTGCTT CATCTCCACT	840
GTGGAATGTA AGGCCGTCAT GGTTTCTTC CACTACTGTG TTGTGTCCAA CTACTTCTGG	900
CTGTTTCATCG AGGGCCTGTA CCTCTTCACT CTGCTGGTGG AGACCTTCTT CCCTGAAAGG	960
AGATACTTCT ACTGGTACAC CATCATTTGGC TGGGGGACCC CAACTGTGTG TGTGACAGTG	1020
TGGGCTACGC TGAGACTCTA CTTTGATGAC ACAGGCTGCT GGGATATGAA TGACAGCACA	1080
GCTCTGTGGT GGGTGATCAA AGGCCCTGTG GTTGGCTCTA TCATGGTTAA CTTTGTGCTT	1140
TTTATTGGCA TTATCGTCAT CCTTGTGCAG AACTTCAGT CTCCAGACAT GGGAGGCAAT	1200

GAGTCCAGCA TCTACTTAAC AAATTTAAGC CCGCGAGTCC CCAAGAAAGC CCGAGAGGAC	1260
CCCCTGCCTG TGCCCTCAGA CCAGCATTC A CTCCCTTTCC TCGGACTGGC CCGGTCCACC	1320
CTGCTGCTCA TCCCCTATT CGGAATCCAC TACACAGTAT TTGCCTTCTC CCCAGAGAAT	1380
GTCAGCAAAA GGGAAAGACT CGTGTTTGAG CTGGGGCTGG GCTCCTTCCA GGGCTTTGTG	1440
GTGGCTGTTC TCTACTGTTT TCTGAATGGT GAGGTACAAG CGGAGATCAA GCGAAAATGG	1500
CGAAGCTGGA AGGTGAACCG TTA CTTCGCT GTGGACTTCA AGCACCGACA CCCGTCTCTG	1560
GCCAGCAGTG GGGTGAATGG GGGCACCCAG CTCTCCATCC TGAGCAAGAG CAGCTCCCAA	1620
ATCCGCATGT CTGGCCTCCC TGCTGACAAT CTGGCCACC	1659

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 498..2036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGGCCTGCAC CCCACCCCCC AGCCTGCGAA GACGGGGGGA GGCGGTGGTC GGTCGCCTCC	60
CTCCTGCCCC CGGCCTGGCT TCGCGGTGGA GGCGGTGCCT CTCCGGCAAG GCAGACCAGG	120
CTGGGCGGAC GCGCGGCGCG GGGCGGGCTA GGAAGGCCG GGGGCCTCGC GCTCGGGCCC	180
CGGGCGGCGA CTGACAGCGG CGGCGGCGGC GGCAGCGGCT CCAAGGCGAG CGTGGTCCCC	240
GCGTGCGCAC AAGCTCGCCG CCGCGCAGGG ACCCACGGAC ACCGGCGCCG GGC GGACACA	300
CAGACGCGGA GATCGGGCTC TACGCGCGCT ACTCAGCGCA CGAGCTCCCC ATCCCTGGGC	360
GGAGCGGGGC GCGGACTCGC CGCTGCGCGC CCTCCCCGCG GAGTCTGCCC CGGGCAGACC	420
CGCAGCCCGC GGCCCCGCCG CGAGGCCCTT GGGTGAGCAG CCTGTAGACA CCTGGGGTTG	480
AGCAGTGGCG GCTGTGAATG AGAGGCGGGC GGC ACTGGCC CGAGCCGCCT TGCAGGCTGA	540

GAAGCGTCAT	GGCCAGCATC	GCGCAGGTCT	CCCTGGCTGC	TCTCCTCCTG	CTGCCTATGG	600
CCACCGCCAT	GCATTCCGAC	TGCATCTTCA	AGAAGGAGCA	AGCCATGTGC	CTGGAGAAGA	660
TCCAGAGGGT	GAATGACCTG	ATGGGCTTGA	ATGACTCCTC	CCCAGGGTGC	CCTGGGATGT	720
GGGACAACAT	CACGTGTTGG	AAGCCCGCCC	ACGTGGGTGA	GATGGTCCTG	GTCAGTTGCC	780
CTGAACTCTT	CCGAATCTTC	AACCCAGACC	AAGTCTGGGA	GACGGAAACC	ATCGGAGAGT	840
TCGGTTTTGC	AGACAGTAAA	TCCTTGGATC	TCTCAGACAT	GAGGGTGGTG	AGCCGGAATT	900
GCACGGAGGA	TGGATGGTCA	GAGCCATTCC	CTCATTATTT	CGATGCCTGT	GGGTTTGAGG	960
AGTACGAATC	TGAGACTGGG	GACCAGGATT	ACTACTACCT	GTCAGTGAAG	GCCCTGTACA	1020
CAGTTGGCTA	CAGCACGTCC	CTCGTCACCC	TCACCACTGC	CATGGTCATC	CTGTGTCGTT	1080
TCCGGAAGCT	GCACTGCACC	CGCAACTTCA	TCCACATGAA	CCTCTTCGTG	TCGTTTATGC	1140
TGAGGGCCAT	CTCCGTCTTC	ATCAAAGACT	GGATCCTCTA	TGCTGAGCAG	GACAGCAATC	1200
ACTGCTTTGT	CTCCACTGTG	GAATGCAAGG	CTGTGATGGT	TTTCTTCCAC	TACTGTGTTG	1260
TATCCAATA	CTTCTGGCTG	TTCATCGAGG	GCCTGTATCT	CTTCACCCTG	CTGGTGGAGA	1320
CCTTCTTCCC	CGAGAGGAGA	TATTTCTACT	GGTACATCAT	CATTGGCTGG	GGGACACCAA	1380
CTGTGTGTGT	GTCTGTGTGG	GCTATGCTGA	GGCTCTACTT	CGATGACACA	GGCTGCTGGG	1440
ATATGAATGA	CAACACGGCT	CTGTGGTGGG	TGATCAAAGG	CCCTGTAGTT	GGCTCCATAA	1500
TGGTTAATTT	TGTGCTCTTC	ATCGGCATCA	TTGTCATCCT	TGTGCAGAAA	CTTCAGTCTC	1560
CAGACATGGG	AGGCAACGAG	TCCAGCATCT	ACTTCAGCTG	CGTGCAGAAA	TGCTACTGCA	1620
AGCCACAGCG	GGCTCAGCAG	CACTCTTGCA	AGATGTCAGA	ACTGTCCACC	ATTACTCTAC	1680
GGCTCGCCAG	GTCCACCTTG	CTGCTCATCC	CACTCTTTGG	AATCCACTAC	ACTGTCTTTG	1740
CTTTCTCCCC	GGAGAACGTC	AGCAAGAGGG	AGAGACTGGT	GTTTGAGCTG	GGTCTGGGCT	1800
CCTTCCAGGG	CTTTGTGGTG	GCTGTTCTCT	ATTGCTTTCT	GAATGGAGAG	GTGCAGGCGG	1860
AGATCAAGAG	GAAGTGGCGG	AGCTGGAAGG	TGAACCGCTA	CTTCACCATG	GACTTCAAGC	1920
ACCGGCACCC	ATCCCTGGCC	AGCAGCGGGG	TGAACGGGGG	CACCCAGCTC	TCCATCCTGA	1980
GCAAGAGCAG	CTCCCAGATC	CGCATGTCTG	GGCTTCCGGC	CGACAACCTG	GCCACCTGAG	2040
CCCACCCTGC	CCCCTCCTCT	CCTCTGTACG	CAGGCTGGGG	CTGTGGTGGG	GCGCCGGCCC	2100

ACGCATGTTG TGCCTCTTCT CGCCTTCGGG CAGGCCCCGG GCTGGGCGCC TGGCCCCCGA	2160
GGTTGGAGAA GGATGCGGGA CAGGCAGCTG TTTAGCCTTC CTGTTTTTGGC GCTGGCCCCAA	2220
CCACCGTGGG TCCCTGGGCC TGCACCCAGA CATGTAATAC TCCTTAATTG GGAAGTCATC	2280
CATTCTTTCC CTTTCCCAAG TCCTTGCTTA TTAAGAGGTT CAAGTCACCT ACCCAATTCA	2340
GAAGCTTAAG TAACCACTAA CCACCGTGAC TGCCTGGGAG GCCTCCCATG GGCTGAGCTA	2400
CTGACTTGGC TTTGGGGGCC TTGGGCTGGG GCCCTCCTTA AAGCCCCCCC TGAAATTGTC	2460
GGACCTCAA GTGTGACTCC TTTGAGTCTA CTCGCCACCC CCGTGGCCCT TTGCAGCCCT	2520
GGTCCAGTCA CCGAGGTTAC TGGAAGTCCA GCTTGGATGG CCAGACAGCT TTTTGGCACA	2580
GGGAGACCCA TGCTCACCCA ACATTTTAGT GTCCAGGTGC CCAGGTGCCC AGGTGCCCAG	2640
CTCCTGGGCA TCAGACAGTG GGAAAGCTCC AGGGATCTAC CATTCAGAGA CTTCAGTTTG	2700
GATGTAGGGC TAAGGCCAGA GAAAAGTTCT GGAGCTTTTC ATTTGGCCCA AGAAAAAACT	2760
GCCAGATCC AGAAAAGTGG ATCTGAGTGG AATTAGATG CAAAGAGCTT GGAG	2814

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2730 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 498..1952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TGGCCTGCAC CCCACCCCCC AGCCTGCGAA GACGGGGGGA GGCGGTGGTC GGTGCGCTCC	60
CTCCTGCCCC CGGCCTGGCT TCGCGGTGGA GGCGGTGCCT CTCCGGCAAG GCAGACCAGG	120
CTGGGCGGAC GCGCGGCGCG GGGCGGGCTA GGGAAGGCCG GGGGCCTCGC GCTCGGGCCC	180
CGGGCGGCGA CTGACAGCGG CGGCGGCGGC GGCAGCGGCT CCAAGGCGAG CGTGGTCCCC	240
GCGTGCGCAC AAGCTCGCCG CCGCGCAGGG ACCCACGGAC ACCGGCGCCG GGCGGACACA	300

CAGACGCGGA GATCGGGCTC TACGCGCGCT ACTCAGCGCA CGAGCTCCCC ATCCCTGGGC	360
GGAGCGGGGC GCGGACTCGC CGCTGCGCGC CCTCCCCGCG GAGTCTGCCC CGGGCAGACC	420
CGCAGCCCCG GGGCCCGCCG CGAGGCCCCCT GGGTGAGCAG CCTGTAGACA CCTGGGGTTG	480
AGCAGTGGCG GCTGTGAATG AGAGGCGGGC GGCAGTGGCC CGAGCCGCCT TGCAGGCTGA	540
GAAGCGTCAT GGCCAGCATC GCGCAGGTCT CCCTGGCTGC TCTCCTCCTG CTGCCTATGG	600
CCACCGCCAT GCATTCCGAC TGCATCTTCA AGAAGGAGCA AGCCATGTGC CTGGAGAAGA	660
TCCAGAGGGT GAATGACCTG ATGGGCTTGA ATGACTCCTC CCCAGGGTGC CCTGGGATGT	720
GGGACAACAT CACGTGTTGG AAGCCCGCCC ACGTGGGTGA GATGGTCCTG GTCAGTTGCC	780
CTGAACTCTT CCGAATCTTC AACCAGACC AAGTCTGGGA GACGGAAACC ATCGGAGAGT	840
TCCGTTTTGC AGACAGTAAA TCCTTGGATC TCTCAGACAT GAGGGTGGTG AGCCGGAATT	900
GCACGGAGGA TGGATGGTCA GAGCCATTCC CTCATTATTT CGATGCCTGT GGGTTTGAGG	960
AGTACGAATC TGAGACTGGG GACCAGGATT ACTACTACCT GTCAGTGAAG GCCCTGTACA	1020
CAGTTGGCTA CAGCACGTCC CTCGTCACCC TCACCACTGC CATGGTCATC CTGTGTCGTT	1080
TCCGGAAGCT GCACTGCACC CGCAACTTCA TCCACATGAA CCTCTTCGTG TCGTTTATGC	1140
TGAGGGCCAT CTCCGTCTTC ATCAAAGACT GGATCCTCTA TGCTGAGCAG GACAGCAATC	1200
ACTGCTTTGT CTCCACTGTG GAATGCAAGG CTGTGATGGT TTTCTTCCAC TACTGTGTTG	1260
TATCCAATA CTTCTGGCTG TTCATCGAGG GCCTGTATCT CTTCAACCCTG CTGGTGGAGA	1320
CCTTCTTCCC CGAGAGGAGA TATTTCTACT GGTACATCAT CATTGGCTGG GGGACACCAA	1380
CTGTGTGTGT GTCTGTGTGG GCTATGCTGA GGCTCTACTT CGATGACACA GGCTGCTGGG	1440
ATATGAATGA CAACACGGCT CTGTGGTGGG TGATCAAAGG CCCTGTAGTT GGCTCCATAA	1500
TGGTTAATTT TGTGCTCTTC ATCGGCATCA TTGTCATCCT TGTGCAGAAA CTTCAGTCTC	1560
CAGACATGGG AGGCAACGAG TCCAGCATCT ACTTACGGCT CGCCAGGTCC ACCTTGCTGC	1620
TCATCCCACT CTTTGGGAATC CACTACACTG TCTTTGCTTT CTCCCCGGAG AACGTCAGCA	1680
AGAGGGAGAG ACTGGTGTTT GAGCTGGGTC TGGGCTCCTT CCAGGGCTTT GTGGTGGCTG	1740
TTCTCTATTG CTTTCTGAAT GGAGAGGTGC AGGCGGAGAT CAAGAGGAAG TGGCGGAGCT	1800
GGAAGGTGAA CCGCTACTTC ACCATGGACT TCAAGCACCG GCACCCATCC CTGGCCAGCA	1860

GCGGGGTGAA CCGGGGCACC CAGCTCTCCA TCCTGAGCAA GAGCAGCTCC CAGATCCGCA	1920
TGTCTGGGCT TCCGGCCGAC AACCTGGCCA CCTGAGCCCA CCCTGCCCCC TCCTCTCCTC	1980
TGTACGCAGG CTGGGGCTGT GGTGGGGCGC CGGCCACGC ATGTTGTGCC TCTTCTCGCC	2040
TTCGGGCAGG CCCCgggCTG GCGCCTGGC CCCCgAGGTT GGAGAAGGAT GCGGGACAGG	2100
CAGCTGTTTA GCCTTCCTGT TTTGGCGCTG GCCCAACCAC CGTGGGTCCC TGGGCCTGCA	2160
CCCAGACATG TAATACTCCT TAATTGGGAA GTCATCCATT CTTTCCCTTT CCCAAGTCCT	2220
TGCTTATTAA GAGGTTCAAG TCACCTACCC AATTCAGAAG CTTAAGTAAC CACTAACCAC	2280
CGTGACTGCG TGGGAGGCCT CCCATGGGCT GAGCTACTGA CTTGGCTTTG GGGGCCTTGG	2340
GCTGGGGCCC TCCTTAAAGC CCCCCCTGAA ATTGTCGGAC CTCAAAGTGT GACTCCTTTG	2400
AGTCTACTCG CCACCCCCGT GGCCCTTTGC AGCCCTGGTC CAGTCACCGA GGTACTGGA	2460
AGTCCAGCTT GGATGGCCAG ACAGCTTTTT GGCACAGGCA GACCCATGCT CACCCAACAT	2520
TTTAGTGTCC AGGTGCCCAG GTGCCCAGGT GCCCAGCTCC TGGGCATCAG ACAGTGGGAA	2580
AGCTCCAGGG ATCTACCATT CAGAGACTTC AGTTTGGATG TAGGGCTAAG GCCAGAGAAA	2640
AGTCTGGAG CTTTTCATTT GGCCCAAGAA AAAACTGCCA AGATCCAGAA AAGTGGATCT	2700
GAGTGGGAATT TAGATGCAAA GAGCTTGGAG	2730

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 77..1477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGAGTGGACA GTGGCAGGCG GTGACTGAAT CTCCAAGTCT GGAAACAATA GCCAGAGATA	60
GTGGCTGGGA AGCACCATGG CCAGAGTCCT GCAGCTCTCC CTGACTGCTC TCCTGCTGCC	120

TGTGGCTATT	GCTATGCACT	CTGACTGCAT	CTTCAAGAAG	GAGCAAGCCA	TGTGCCTGGA	180
GAGGATCCAG	AGGGCCAACG	ACCTGATGGG	ACTAAACGAG	TCTTCCCCAG	GTTGCCCTGG	240
CATGTGGGAC	AATATCACAT	GTTGGAAGCC	AGCTCAAGTA	GGTGAGATGG	TCCTTGTAAG	300
CTGCCCTGAG	GTCTTCCGGA	TCTTCAACCC	GGACCAAGTC	TGGATGACAG	AAACCATAGG	360
AGATTCTGGT	TTTGCCGATA	GTAATTCCTT	GGAGATCACA	GACATGGGGG	TCGTGGGCCG	420
GAAGTGCACA	GAGGACGGCT	GGTCGGAGCC	CTTCCCCCAC	TACTTCGATG	CTTGTGGGTT	480
TGATGATTAT	GAGCCTGAGT	CTGGAGATCA	GGATTATTAC	TACCTGTCGG	TGAAGGCTCT	540
CTACACAGTC	GGCTACAGCA	CTTCCCTCGC	CACCCTCACT	ACTGCCATGG	TCATCTTGTC	600
CCGCTTCCGG	AAGCTGCATT	GCACTCGCAA	CTTCATCCAC	ATGAACCTGT	TTGTATCCTT	660
CATGCTGAGG	GCTATCTCCG	TCTTCATCAA	GGACTGGATC	TTGTACGCCG	AGCAGGACAG	720
CAGTCACTGC	TTCGTTTCCA	CCGTGGAGTG	CAAAGCTGTC	ATGGTTTTCT	TCCACTACTG	780
CGTGGTGTCC	AACTACTTCT	GGCTGTTCAT	TGAAGGCCTG	TACCTCTTTA	CACTGCTGGT	840
GGAGACCTTC	TTCCCTGAGA	GGAGATATTT	CTACTGGTAC	ACCATCATCG	GCTGGGGGAC	900
ACCTACTGTG	TGTGTAAACAG	TGTGGGCTGT	GCTGAGGCTC	TATTTTGATG	ATGCAGGATG	960
CTGGGATATG	AATGACAGCA	CAGCTCTGTG	GTGGGTGATC	AAAGGCCCCG	TGGTTGGCTC	1020
TATAATGGTT	AACTTTGTGC	TTTTCATCGG	CATCATCATC	ATCCTTGATC	AGAAGCTGCA	1080
GTCCCCAGAC	ATGGGAGGCA	ACGAGTCCAG	CATCTACTTA	CGGCTGGCCC	GCTCCACCCT	1140
ACTGCTCATC	CCACTCTTCG	GAATCCACTA	CACAGTATTC	GCCTTCTCTC	CAGAGAACGT	1200
CAGCAAGAGG	GAAAGACTTG	TGTTTGAGCT	TGGGCTGGGC	TCCTTCCAGG	GCTTTGTGGT	1260
GGCTGTACTC	TACTGCTTCC	TGAATGGGGA	GGTACAGGCA	GAGATTAAGA	GGAAATGGAG	1320
GAGCTGGAAG	GTGAACCGTT	ACTTCACTAT	GGACTTCAAG	CACCGGCACC	CGTCCCTGGC	1380
CAGCAGTGA	GTAAATGGGG	GAACCCAGCT	GTCCATCCTG	AGCAAGAGCA	GCTCCCAGCT	1440
CCGCATGTCC	AGCCTCCCGG	CCGACAACTT	GGCCACCTGA	GGCCTGTCTC	CCTCCTCCTT	1500
CTGCACAGGC	TGGGGCTGCG	GGCCAGTGCC	TGAGCATGTT	TGTGCCTCTC	CCCTCTCCTT	1560
GGGCAGGCCC	TGGGTAGGAA	GCTGGGCTCC	TCCCCAAAGG	GGAAGAGAGA	GATAGGGTAT	1620
AGGCTGATAT	TGCTCCTCCT	GTTTGGGTCC	CACCTACTGT	GATTCATTGA	GCCTGATTTG	1680

ACATGTAAAT ACACCTCAAA TTTGGAAAGT TGCCCCATCT CTGCCCCCAA CCCATGCCCC	1740
TGCTCACCTC TGCCAGGCCC CAGCTCAACC TACTGTGTCA AGGCCAGCCT CAGTGATAGT	1800
CTGATCCCAG GTACAAGGCC TTGTGAGCTG AGGCTGAAAG GCCTGTTTTG GAGAGGCTGG	1860
GGTAGTGCC	1869

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 77..1561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CGAGTGGACA GTGGCAGGCG GTGACTGAAT CTCCAAGTCT GGAAACAATA GCCAGAGATA	60
GTGGCTGGGA AGCACCATGG CCAGAGTCCT GCAGCTCTCC CTGACTGCTC TCCTGCTGCC	120
TGTGGCTATT GCTATGCACT CTGACTGCAT CTTCAAGAAG GAGCAAGCCA TGTGCCTGGA	180
GAGGATCCAG AGGGCCAACG ACCTGATGGG ACTAAACGAG TCTTCCCCAG GTTGCCCTGG	240
CATGTGGGAC AATATCACAT GTTGGAAGCC AGCTCAAGTA GGTGAGATGG TECTTGTAAG	300
CTGCCCTGAG GTCTTCCGGA TCTTCAACCC GGACCAAGTC TGGATGACAG AAACCATAGG	360
AGATTCTGGT TTTGCCGATA GTAATTCCTT GGAGATCACA GACATGGGGG TCGTGGGCCG	420
GAACTGCACA GAGGACGGCT GGTCCGAGCC CTTCCCCCAC TACTTCGATG CTTGTGGGTT	480
TGATGATTAT GAGCCTGAGT CTGGAGATCA GGATTATTAC TACCTGTCGG TGAAGGCTCT	540
CTACACAGTC GGCTACAGCA CTTCCCTCGC CACCCTCACT ACTGCCATGG TCATCTTGTT	600
CCGCTTCCGG AAGCTGCATT GCACTCGCAA CTTTCATCCAC ATGAACCTGT TTGTATCCTT	660
CATGCTGAGG GCTATCTCCG TCTTCATCAA GGACTGGATC TTGTACGCCG AGCAGGACAG	720
CAGTCACTGC TTCGTTTCCA CCGTGGAGTG CAAAGCTGTC ATGGTTTCT TCCACTACTG	780

CGTGGTGTCC	AACTACTTCT	GGCTGTTCAT	TGAAGGCCTG	TACCTCTTTA	CACTGCTGGT	840
GGAGACCTTC	TTCCCTGAGA	GGAGATATTT	CTACTGGTAC	ACCATCATCG	GCTGGGGGAC	900
ACCTACTGTG	TGTGTAACAG	TGTGGGCTGT	GCTGAGGCTC	TATTTTGATG	ATGCAGGATG	960
CTGGGATATG	AATGACAGCA	CAGCTCTGTG	GTGGGTGATC	AAAGGCCCCG	TGGTTGGCTC	1020
TATAATGGTT	AACTTTGTGC	TTTTCATCGG	CATCATCATC	ATCCTTGTAC	AGAAGCTGCA	1080
GTCCCCAGAC	ATGGGAGGCA	ACGAGTCCAG	CATCTACTTC	AGCTGCGTGC	AGAAATGCTA	1140
CTGCAAGCCA	CAGCGGGCTC	AGCAGCACTC	TTGCAAGATG	TCAGAACTAT	CCACCATTAC	1200
TCTACGGCTG	GCCCGCTCCA	CCCTACTGCT	CATCCCACTC	TTCGGAATCC	ACTACACAGT	1260
ATTGCGCTTC	TCTCCAGAGA	ACGTCAGCAA	GAGGGAAAGA	CTTGTGTTTG	AGCTTGGGCT	1320
GGCTCCTTC	CAGGGCTTTG	TGGTGGCTGT	ACTCTACTGC	TTCCTGAATG	GGGAGGTACA	1380
GGCAGAGATT	AAGAGGAAAT	GGAGGAGCTG	GAAGGTGAAC	CGTTACTTCA	CTATGGACTT	1440
CAAGCACCGG	CACCCGTCCC	TGGCCAGCAG	TGGAGTAAAT	GGGGGAACCC	AGCTGTCCAT	1500
CCTGAGCAAG	AGCAGCTCCC	AGCTCCGCAT	GTCCAGCCTC	CCGGCCGACA	ACTTGGCCAC	1560
CTGAGGCCTG	TCTCCCTCCT	CCTTCTGCAC	AGGCTGGGGC	TGCGGGCCAG	TGCCTGAGCA	1620
TGTTTG TGCC	TCTCCCCTCT	CCTTGGGCAG	GCCCTGGGTA	GGAAGCTGGG	CTCCTCCCCA	1680
AAGGGGAAGA	GAGAGATAGG	GTATAGGCTG	ATATTGCTCC	TCCTGTTTGG	GTCCACCTA	1740
CTGTGATTCA	TTGAGCCTGA	TTTGACATGT	AAATACACCT	CAAATTTGGA	AAGTTGCCCC	1800
ATCTCTGCCC	CCAACCCATG	CCCCTGCTCA	CCTCTGCCAG	GCCCCAGCTC	AACCTACTGT	1860
GTCAAGGCCA	GCCTCAGTGA	TAGTCTGATC	CCAGGTACAA	GGCCTTGTGA	GCTGAGGCTG	1920
AAAGGCCTGT	TTTGGAGAGG	CTGGGGTAGT	GCCCACCCCA	GCAGCCTTTC	AGCAAATTGA	1980
CTTTGGATGT	GGACCCTTCT	CAGCCTGTAC	CAAGTACTGC	AGTTGGCTAG	GGATGCAGCT	2040
CAGTTTCCTG	AGCATCCTTT	GGAGCAGGTC	AACCTGAGGC	TCCTTTTGCT	TACCCGACAT	2100
CTAAGTTGTC	CAGGTGCTCG	GCTCCTGTGT	GCCTGGATGA	CGGGAGGGCT	CCGGGGTCTT	2160
TCAGTCAAAG	ACTTACATTG	AGGTGGGGTG	AGAGTCAGAG	AAAAGTTCTG	GTGCTTTTCA	2220
TTTGTTCCTA	GAGCTGAGAG	CCAGGAATGC	AGAGTCAATT	GGGAAGGAGA	TGGGATAGCT	2280
GATGATCTTA	CCATGTCCAT	GACTGTGCCC	CTGATTCAAG	ACCGGATCAT	GTGGTGGCTT	2340

TATTTCTACA CTTCTTGTCC ACAATGGACA GTCTGAGGAA GCTCTTCTTT CAGCCACAAC 2400
 AACCACAGAA AGCCCTTTCT TCTCCCCTCT TGTTTCTCCA TAAGTCAAAG CCATGTTTAG 2460
 AACGGACCAG CCACCTTGCG ATGAAATCAC TGAGTTCTGA AGCAACTTTC AATTTCCACG 2520
 AGCCAAGTCC TGGGTCCAGG GACGCCCC 2548

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 74..1648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AGGCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG 60
 GCCAAGAAGT GTCATGGCTG GTGTCGTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCCTG 120
 TCCGTGGGGC CGGGGCAGAC TCCGCAAAGG ACGCGCAGCC TGCAAGTCCG CGGCCAGAG 180
 ACACATTGGG GCTGACCTGC CGCTGCTGTC AGTGGGAGGC CAGTGGTGCT GGCCAAGAAG 240
 TGTCATGGCT GGTGTCGTGC ACGTTTCCCT GGCTGCTCTC CTCCTGCTGC CTATGGCCCC 300
 TGCCATGCAT TCTGACTGCA TCTTCAAGAA GGAGCAAGCC ATGTGCCTGG AGAAGATCCA 360
 GAGGGCCAAT GAGCTGATGG GCTTCAATGA TTCCTCTCCA GGCTGTCCTG GGATGTGGGA 420
 CAACATCACG TGTTGGAAGC CCGCCCATGT GGGTGAGATG GTCCTGGTCA GCTGCCCTGA 480
 GCTCTTCCGA ATCTTCAACC CAGACCAAGT CTGGGAGACC GAAACCATTG GAGAGTCTGA 540
 TTTTGGTGAC AGTAACTCCT TAGATCTCTC AGACATGGGA GTGGTGAGCC GGAAGTGCAC 600
 GGAGGATGGC TGGTCGGAAC CCTTCCCTCA TTAATTTGAT GCCTGTGGGT TTGATGAATA 660
 TGAATCTGAG ACTGGGGACC AGGATTATTA CTACCTGTCA GTGAAGGCCC TCTACACGGT 720
 TGGCTACAGC ACATCCCTCG TCACCCTCAC CACTGCCATG GTCATCCTTT GTCGCTTCCG 780

GAAGCTGCAC TGCACACGCA ACTTCATCCA CATGAACCTG TTTGTGTCGT TCATGCTGAG	840
GGCGATCTCC GTCTTCATCA AAGACTGGAT TCTGTATGCG GAGCAGGACA GCAACCACTG	900
CTTCATCTCC ACTGTGGAAT GTAAGGCCGT CATGGTTTTTTC TTCCACTACT GTGTTGTGTC	960
CAACTACTTC TGGCTGTTCA TCGAGGGCCT GTACCTCTTC ACTCTGCTGG TGGAGACCTT	1020
CTTCCCTGAA AGGAGATACT TCTACTGGTA CACCATCATT GGCTGGGGGT CCCCAACTGT	1080
GTGTGTGACA GTGTGGGCTA CGCTGAGACT CTACTTTGAT GACACAGGCT GCTGGGATAT	1140
GAATGACAGC ACAGCTCTGT GGTGGGTGAT CAAAGGCCCT GTGGTTGGCT CTATCATGGT	1200
TAACCTTTGTG CTTTTTATTG GCATTATCGT CATCCTTGTG CAGAACTTC AGTCTCCAGA	1260
CATGGGAGGC AATGAGTCCA GCATCTACTT GCGACTGGCC CGGTCCACCC TGCTGCTCAT	1320
CCCCTATTTC GGAATCCACT ACACAGTATT TGCCTTCTCC CCAGAGAATG TCAGCAAAAG	1380
GGAAAGACTC GTGTTTGAGC TGGGGCTGGG CTCCTTCCAG GGCTTTGTGG TGGCTGTTCT	1440
CTACTGTTTT CTGAATGGTG AGGTACAAGC GGAGATCAAG CGAAAATGGC GAAGCTGGAA	1500
GGTGAACCGT TACTTCGCTG TGGACTTCAA GCACCGACAC CCGTCTCTGG CCAGCAGTGG	1560
GGTGAATGGG GGCACCCAGC TCTCCATCCT GAGCAAGAGC AGCTCCCAA TCCGCATGTC	1620
TGGCCTCCCT GCTGACAATC TGGCCACCTG AGCCATGCTC CCCT	1664

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 74..1732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG	60
GCCAAGAAGT GTCATGGCTG GTGTCGTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCCTG	120

TCCGTGGGGC	CGGGGCAGAC	TCCGCAAAGG	ACGCGCAGCC	TGCAAGTCCG	CGGCCCAGAG	180
ACACATTGGG	GCTGACCTGC	CGCTGCTGTC	AGTGGGAGGC	CAGTGGTGCT	GGCCAAGAAG	240
TGTCATGGCT	GGTGTCTGTC	ACGTTTCCCT	GGCTGCTCTC	CTCCTGCTGC	CTATGGCCCC	300
TGCCATGCAT	TCTGACTGCA	TCTTCAAGAA	GGAGCAAGCC	ATGTGCCTGG	AGAAGATCCA	360
GAGGGCCAAT	GAGCTGATGG	GCTTCAATGA	TTCCTCTCCA	GGCTGTCCTG	GGATGTGGGA	420
CAACATCACG	TGTTGGAAGC	CCGCCCATGT	GGGTGAGATG	GTCCTGGTCA	GCTGCCCTGA	480
GCTCTTCCGA	ATCTTCAACC	CAGACCAAGT	CTGGGAGACC	GAAACCATTG	GAGAGTCTGA	540
TTTTGGTGAC	AGTAACTCCT	TAGATCTCTC	AGACATGGGA	GTGGTGAGCC	GGAAGTGCAC	600
GGAGGATGGC	TGGTCGGAAC	CCTTCCCTCA	TTACTTTGAT	GCCTGTGGGT	TTGATGAATA	660
TGAATCTGAG	ACTGGGGACC	AGGATTATTA	CTACCTGTCA	GTGAAGGCCC	TCTACACGGT	720
TGGCTACAGC	ACATCCCTCG	TCACCCTCAC	CACTGCCATG	GTCATCCTTT	GTCGCTTCCG	780
GAAGCTGCAC	TGCACACGCA	ACTTCATCCA	CATGAACCTG	TTTGTGTCGT	TCATGCTGAG	840
GGGATCTCC	GTCTTCATCA	AAGACTGGAT	TCTGTATGCG	GAGCAGGACA	GCAACCACTG	900
CTTCATCTCC	ACTGTGGAAT	GTAAGGCCGT	CATGGTTTTT	TTCCACTACT	GTGTTGTGTC	960
CAACTACTTC	TGGCTGTTCA	TCGAGGGCCT	GTACCTCTTC	ACTCTGCTGG	TGGAGACCTT	1020
CTTCCCTGAA	AGGAGATACT	TCTACTGGTA	CACCATCATT	GGCTGGGGGA	CCCCAACTGT	1080
GTGTGTGACA	GTGTGGGCTA	CGCTGAGACT	CTACTTTGAT	GACACAGGCT	GCTGGGATAT	1140
GAATGACAGC	ACAGCTCTGT	GGTGGGTGAT	CAAAGGCCCT	GTGGTTGGCT	CTATCATGGT	1200
TAACTTTGTG	CTTTTTATTG	GCATTATCGT	CATCCTTGTG	CAGAAACTTC	AGTCTCCAGA	1260
CATGGGAGGC	AATGAGTCCA	GCATCTACTT	CAGCTGCGTG	CAGAAATGCT	ACTGCAAGCC	1320
ACAGCGGGCT	CAGCAGCACT	CTTGCAAGAT	GTCAGAACTG	TCCACCATTA	CTCTGCGACT	1380
GGCCCGGTCC	ACCCTGCTGC	TCATCCCACT	ATTCGGAATC	CACTACACAG	TATTTGCCTT	1440
CTCCCCAGAG	AATGTCAGCA	AAAGGGAAAG	ACTCGTGTTT	GAGCTGGGGC	TGGGCTCCTT	1500
CCAGGGCTTT	GTGGTGGCTG	TTCTCTACTG	TTTTCTGAAT	GGTGAGGTAC	AAGCGGAGAT	1560
CAAGCGAAAA	TGGCGAAGCT	GGAAGGTGAA	CCGTTACTTC	GCTGTGGACT	TCAAGCACCG	1620
ACACCCGTCT	CTGGCCAGCA	GTGGGGTGAA	TGGGGGCACC	CAGCTCTCCA	TCCTGAGCAA	1680

GAGCAGCTCC CAAATCCGCA TGTCTGGCCT CCCTGCTGAC AATCTGGCCA CCTGAGCCAT 1740
GCTCCCCCT 1748

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 74..1729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AGCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG 60
GCCAAGAAGT GTCATGGCTG GTGTCGTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCCTG 120
TCCGTGGGGC CGGGGCAGAC TCCGCAAAGG ACGCGCAGCC TGCAAGTCCG CGGCCAGAG 180
ACACATTGGG GCTGACCTGC CGCTGCTGTC AGTGGGAGGC CAGTGGTGCT GGCCAAGAAG 240
TGTCATGGCT GGTGTCGTGC ACGTTTCCCT GGCTGCTCTC CTCCTGCTGC CTATGGCCCC 300
TGCCATGCAT TCTGACTGCA TCTTCAAGAA GGAGCAAGCC ATGTGCCTGG AGAAGATCCA 360
GAGGGCCAAT GAGCTGATGG GCTTCAATGA TTCCTCTCCA GGCTGTCCTG GGATGTGGGA 420
CAACATCACG TGTTGGAAGC CCGCCCATGT GGGTGAGATG GTCCTGGTCA GCTGCCCTGA 480
GCTCTTCCGA ATCTTCAACC CAGACCAAGT CTGGGAGACC GAAACCATTG GAGAGTCTGA 540
TTTTGGTGAC AGTAACTCCT TAGATCTCTC AGACATGGGA GTGGTGAGCC GGAAGTGCAC 600
GGAGGATGGC TGGTCGGAAC CCTTCCCTCA TTACTTTGAT GCCTGTGGGT TTGATGAATA 660
TGAATCTGAG ACTGGGGACC AGGATTATTA CTACCTGTCA GTGAAGGCC TCTACACGGT 720
TGGCTACAGC ACATCCCTCG TCACCCTCAC CACTGCCATG GTCATCCTTT GTCGCTTCCG 780
GAAGCTGCAC TGCACACGCA ACTTCATCCA CATGAACCTG TTTGTGTCGT TCATGCTGAG 840
GGCGATCTCC GTCTTCATCA AAGACTGGAT TCTGTATGCG GAGCAGGACA GCAACCACTG 900

CTTCATCTCC ACTGTGGAAT GTAAGGCCGT CATGGTTTTTTC TTCCACTACT GTGTTGTGTC 960
 CAACTACTTC TGGCTGTTCA TCGAGGGCCT GTACCTCTTC ACTCTGCTGG TGGAGACCTT 1020
 CTTCCCTGAA AGGAGATACT TCTACTGGTA CACCATCATT GGCTGGGGGA CCCCAACTGT 1080
 GTGTGTGACA GTGTGGGCTA CGCTGAGACT CTACTTTGAT GACACAGGCT GCTGGGATAT 1140
 GAATGACAGC ACAGCTCTGT GGTGGGTGAT CAAAGGCCCT GTGGTTGGCT CTATCATGGT 1200
 TAACTTTGTG CTTTTTATTG GCATTATCGT CATCCTTG TG CAGAAACTTC AGTCTCCAGA 1260
 CATGGGAGGC AATGAGTCCA GCATCTACTT CTGCGTGCAG AAATGCTACT GCAAGCCACA 1320
 GCGGGCTCAG CAGCACTCTT GCAAGATGTC AGAACTGTCC ACCATTACTC TCGGACTGGC 1380
 CCGGTCCACC CTGCTGCTCA TCCCCTATT CGGAATCCAC TACACAGTAT TTGCCTTCTC 1440
 CCCAGAGAAT GTCAGCAAAA GGGAAAGACT CGTGTTTGAG CTGGGGCTGG GCTCCTTCCA 1500
 GGGCTTTGTG GTGGCTGTTC TCTACTGTTT TCTGAATGGT GAGGTACAAG CGGAGATCAA 1560
 GCGAAAATGG CGAAGCTGGA AGGTGAACCG TTA CTTCGCT GTGGACTTCA AGCACCGACA 1620
 CCCGTCTCTG GCCAGCAGTG GGGTGAATGG GGGCACCCAG CTCTCCATCC TGAGCAAGAG 1680
 CAGCTCCCAA ATCCGCATGT CTGGCCTCCC TGCTGACAAT CTGGCCACCT GAGCCATGCT 1740
 CCCCT 1745

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 74..1732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AGCCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGCTG 60
 GCCAAGAAGT GTCATGGCTG GTGTCGTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCCTG 120

TCCGTGGGGC	CGGGGCAGAC	TCCGCAAAGG	ACGCGCAGCC	TGCAAGTCCG	CGGCCCAGAG	180
ACACATTGGG	GCTGACCTGC	CGCTGCTGTC	AGTGGGAGGC	CAGTGGTGCT	GGCCAAGAAG	240
TGTCATGGCT	GGTGTCTGTC	ACGTTTCCCT	GGCTGCTCTC	CTCCTGCTGC	CTATGGCCCC	300
TGCCATGCAT	TCTGACTGCA	TCTTCAAGAA	GGAGCAAGCC	ATGTGCCTGG	AGAAGATCCA	360
GAGGGCCAAT	GAGCTGATGG	GCTTCAATGA	TTCCTCTCCA	GGCTGTCCTG	GGATGTGGGA	420
CAACATCACG	TGTTGGAAGC	CCGCCCATGT	GGGTGAGATG	GTCCTGGTCA	GCTGCCCTGA	480
GCTCTTCCGA	ATCTTCAACC	CAGACCAAGT	CTGGGAGACC	GAAACCATTG	GAGAGTCTGA	540
TTTTGGTGAC	AGTAACTCCT	TAGATCTCTC	AGACATGGGA	GTGGTGAGCC	GGAAGTGCAC	600
GGAGGATGGC	TGGTCGGAAC	CCTTCCCTCA	TTACTTTGAT	GCCTGTGGGT	TTGATGAATA	660
TGAATCTGAG	ACTGGGGACC	AGGATTATTA	CTACCTGTCA	GTGAAGGCC	TCTACACGGT	720
TGGCTACAGC	ACATCCCTCG	TCACCCTCAC	CACTGCCATG	GTCATCCTTT	GTCGCTTCCG	780
GAAGCTGCAC	TGCACACGCA	ACTTCATCCA	CATGAACCTG	TTTGTGTCGT	TCATGCTGAG	840
GGGATCTCC	GTCTTCATCA	AAGACTGGAT	TCTGTATGCG	GAGCAGGACA	GCAACCACTG	900
CTTCATCTCC	ACTGTGGAAT	GTAAGGCCGT	CATGGTTTTT	TTCCACTACT	GTGTTGTGTC	960
CAACTACTTC	TGGCTGTTCA	TCGAGGGCCT	GTACCTCTTC	ACTCTGCTGG	TGGAGACCTT	1020
CTTCCCTGAA	AGGAGATACT	TCTACTGGTA	CACCATCATT	GGCTGGGGGA	CCCCAACTGT	1080
GTGTGTGACA	GTGTGGGCTA	CGCTGAGACT	CTACTTTGAT	GACACAGGCT	GCTGGGATAT	1140
GAATGACAGC	ACAGCTCTGT	GGTGGGTGAT	CAAAGGCCCT	GTGGTTGGCT	CTATCATGGT	1200
TAACTTTGTG	CTTTTTATTG	GCATTATCGT	CATCCTTGTG	CAGAACTTC	AGTCTCCAGA	1260
CATGGGAGGC	AATGAGTCCA	GCATCTACTT	AACAAATTTA	AGCCCGCGAG	TCCCCAAGAA	1320
AGCCCGAGAG	GACCCCCTGC	CTGTGCCCTC	AGACCAGCAT	TACTCCCTT	TCCTGCGACT	1380
GGCCCGGTCC	ACCCTGCTGC	TCATCCCACT	ATTCGGAATC	CACTACACAG	TATTTGCCTT	1440
CTCCCCAGAG	AATGTCAGCA	AAAGGGAAAG	ACTCGTGTTT	GAGCTGGGGC	TGGGCTCCTT	1500
CCAGGGCTTT	GTGGTGGCTG	TTCTCTACTG	TTTTCTGAAT	GGTGAGGTAC	AAGCGGAGAT	1560
CAAGCGAAAA	TGGCGAAGCT	GGAAGGTGAA	CCGTTACTTC	GCTGTGGACT	TCAAGCACCG	1620
ACACCCGTCT	CTGGCCAGCA	GTGGGGTGAA	TGGGGGCACC	CAGCTCTCCA	TCCTGAGCAA	1680

GAGCAGCTCC CAAATCCGCA TGTCTGGCCT CCCTGCTGAC AATCTGGCCA CCTGAGCCAT 1740
GCTCCCCT 1748

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

His Ser Asp Gly Ile Phe Thr Asp Ser Tyr Ser Arg Tyr Arg Lys Gln
1 5 10 15
Met Ala Val Lys Lys Tyr Leu Ala Ala Val Leu Gly Lys Arg Tyr Lys
20 25 30
Gln Arg Val Lys Asn Lys
35

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

His Ser Asp Gly Ile Phe Thr Asp Ser Tyr Ser Arg Tyr Arg Lys Gln
1 5 10 15
Met Ala Val Lys Lys Tyr Leu Ala Ala Val Leu
20 25

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CAGAAAGCTT CGGACCATGC GCCCTCCGAG CCCACCG

37

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGGCTCTAGA CGGTCAGACC AGGGAGACCT CCGCTTG

37

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu	Lys	Ile	Gln
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TGGATCTTCT CCAGGTGCAT DGCCTGCTCC TTCTTGAAGA TGTGGTC

47

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTGGGATATG AATGACAGCA CAGC

24

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TCTGGGGAGA AGGCAAATAC TGTG

24

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid, Synthetic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TGCGTGCGA AATGCTACTG CAAGCCACAG

30

